ZŠTIC-Biotech/ChemLib

92655

From: Sent: To: Subj ct:

Mehta, Ashwin Monday, April 28, 2003 4:11 PM STIC-Biotech/ChemLib sequence search

STIC,

Please search the commercial and interference databases for the following from 09/845,849:

1) the nucleotide sequence of SEQ ID NO: 1

2) the nucleotide sequence of SEQ ID NO: 3

My mail room is 9E12, office 9E07, art unit 1638.

Thank you, Ashwin

Ashwin Mehta United States Patent and Trademark Office Biotechnology Patent Examiner 703-306-4540 Chi.

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: 424
Date Completed: 156
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
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Pred. No. is the number of results predicted by chance to have

REFERENCE AUTHORS

TITLE JOURNAL

1 (bases 1 to 856) weigel, D. and Kardailsky, I. Flowering locus T (FT) and genetically modified plants having modulated flower development Patent: US 6225530-A 3 01-MAY-2001;

SOURCE ORGANISM

Unknown. Unknown. Unclassified.

VERSION KEYWORDS

RESULT 1
AR148907/c
LOCUS
DEFINITION
ACCESSION

AR148907 Sequence 3 : AR148907 AR148907.1

from patent US GI:15112997

856 bp s 6225530.

DNA

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08-AUG-2001

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Araki, T. and Kobayashi, Y.

Direct Submission

Submitted (19-MAY -1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:taraquiegr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136, Fax:81-75-753-4141)
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flowering signals
Science 286 (5446), 1960-1962 (1999)
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/td_xref="GI:4903012"
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/db_xref="taxon:3702"
/chromosome="1"
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11596-11657, 12371-12411, and 12536-13005 of i
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REFERENCE AUTHORS VERSION KEYWORDS DEFINITION SOURCE ACCESSION ORGANISM Arabidopsis thaliana. Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. AY065378.1 FLI_CDNA. Arabidopsis thaliana FT (At1965480) mRNA, AY065378 AY065378 (bases 1 to 840) ada, K., Liu, S.X., 840 bp mRNA putative flowering complete cds. signals Linear mediating PLN 26-APR-2002 protein

Sakano, H.,

Pham, P.K.,

Banh, J.,

Chung, M.K.

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767; Conserv
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2 (bases 1 to 840)

Yamada, K., Banh, J., Chang, C.H., Chang, E., Dale, J.M.,

Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,

Goldsmith, Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,

Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawati, Y., Kim, C., Lam, B.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawati, J., Kim, C., Lam, B.,

Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,

Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,

Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94/710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L. Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T. Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamadà,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium
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                                                                                                                                                                                                                                         /product="putative flowering signals mediating protein FT"
/protein_id="AAL38819.1"
/protein_id="AAL38819.1"
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NEIVCYENPSPTAGIHRVVFILFRQLGRQTVYAPGWRONFNTREFAEIYNLGLPVAAV
FYNCQRESGCGGRRL"
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83..6
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(Lambda ZAP) as a XhoI/SstI insert.
ecotype: Columbia"
                                                                                                                                                                             /gene="At1g65480"
148 c 182
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/db_xref="taxon:3702"
/chromosome="1"
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Araki,T. and Kobayashi,
Direct Submission
                                                                                     flowering signals
Science 286 (5446)
                                                                                                                                Kobayashi,Y., Kaya,H., Goto,K., Twabuchi,M. and Araki,T. A pair of related genes with antagonistic roles in media
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:taraqui@gr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136, Fax:81-75-753-4141)
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/note="amino acid residues 1-101 of hypothetical
translation product are identical to those of FT
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/db_xref="GI:4903014"
/translation="MSINIEDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLR
PSQVQNKPRVEIGGEDLRNFYTLVMVDPDVPSPSNPHLREYLHWLVTDIPATTGTTFA
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/strain="Landsberg er"
/db_xref="taxon:3702"
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1 (bases 1 to 559)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V. Yamada, K., Chan, M.M., Chang, C.C., Toriumi, M., Wallender, E.K., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H. Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Ngyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
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Arabidopsis thaliana
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida. Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                 Submitted (17-JUL-2002) Plant Gene Expression Center, Street, Albany, CA 94710, USA
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The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CNNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G., Yuan,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally

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                  TTTATAACCAATTGATATT
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          TTTATAACCAATTGATATT
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/db_xref="taxon:3702"
/chromosome="1"
/clone="U11796"
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Method
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Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.
Method for shortening plant generation and plant
Patent: JP 2000139250 A 1 23-MAY-2000;
TORAY IND INC
OS Arabidopsis
PN JP 2000139250-A/1
PD 23-MAY-2000
PF 11-NOV-1998 JP 1998320219
PR
                                                                                                                      CTCAGGAACTTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACCCT
                                                                                                                                                                                                                                                                                                                                                                          ATGTCTATAAATATAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGAT
             AACTTCAACACTCGCGAGTTTGCTGAGATCTACAATCTCGGCCTTCCCGTGGCCGCAGTT
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                                                             GTGTTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAG
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E38985.1 GI:186250
JP 2000139250-A/1.
Arabidopsis.
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CC
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FH Key Location/Qualifiers
FT source 1.528
FT source /organism-'Arabidopsis'.
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Eukaryota;
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1 (bases 1 to 528)
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Location/Qualifiers
1. .528
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/db_xref="taxon:3701"
111 c 129 g 1
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Pred. No. 2.4e-114;
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	/db_xret="G1:2190555" /translation="marqpkselfpkikisTNSGVTSDGEPNMEKQGDGCEENNFDGR OCKPSSGNRKKSRRVKOLLOFFNKGCRDGEPKIKISTNSGVTSTILLTKOLLTKILLVEK	
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	complement(]oin(129327,9501191)) /gene="F5114.1" /codon start=1	CDS
		gene
	/db_xref="taxon:3702" /chromosome="1" ·	
	/organism="Arabidopsis thaliana" /cultivar="Columbia"	
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	On Jun 10, 1997 this sequence version replaced gi:1943864.	COMMENT
	Direct Submission Submitted (11-JUN-1997)	TITLE JOURNAL
	Theologis, A.	AUTHORS
	Street, Albany, CA 94710, USA 5 (bases 1 to 109560)	REFERENCE
		JOURNAL
		AUTHORS
		REFERENCE
	Submitted (1-APR-1997) Plant Gene Expression Center, 800 Buchanan	JOURNAL
		AUTHORS
		REFERENCE
	Submitted (15-APR-1997) Plant Gene Expression Center, 800 Buchanan	JOURNAL
	Theologis, A. Direct Submission	TITLE
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		JOURNAL
		7 17 1
	Sieu, 1. N., Bueillei, E., Conway, A.B., Conway, A.K., Dewar, K., Feng, J., Kim, C., Kurtz, D., Li, Y., Shinn, P., Sun, H., Davis, R.W., Ecker, J.R.,	
		AUTHORS
		REFERENCE
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	Arabidopsis thaliana	ORGANISM
	Arabidopsis	SOURCE
	AC001229 AC001229.1 GI:2182285	VERSION VERSION
	complete sequence.	NOTOBECON
	F5I14 109560 bp DNA linear PLN 11-JUN-1997 N Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1,	LOCUS DEFINITION
		RESULT 8 F5I14
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		481
	TTCTACAATTGTCAGAGGGAGAGTGGCTGCGGAGGAAGAAGACTTTAG 590	Оу 543

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KLANGKGLSRRERQQLTRTTADIFRLVPVAVFIIVPFMEFLLPVFLKLFPNMLPSTFQ DKMKEEEALKRRLNARMEYAKFLQDTVKEMAKEVQTSRSGEIKKTAEDLDGFMTKVRR

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OKAIADKTSSALLDRVETMLQKLEKEIDDVDNKIGNRWRLLDRSVDYDGKVSPDEVAL YLKLKEKTESYTMVAVKSAVVSVGQRVSYGVLNVDADVLEDDSESCLMCWETRDLKIM PSSVRGVLKLARTCRKKIHERITAVSAMLAALQREETEKLMKSDLSKAAEKLGKILSE VDIRSFMDNMAQKNSSEMAEKDSKREEKLLKQLEKNCLEKNCEAEKEKKRMERQVLKEKLG QEKEQKILQKAIVDENNKEKEETESKRIKQQDESEKEQKREKEQAELKOLQVQK QASIMERFLKKSKDSLTQPKLPSSEVTAQELSCTKHENEIGKVVQAIDNAFSTTCEA /translation="megfyrsrllqspsfsngvgilelpyplgyrlvfqsmysslata NKPDHDKKGEKVTSQTKEASPEECDEAVEGLSLAKAKAKKLEESQKSDISIMQRVR LFLLGIGPALRAIASMSREDMAKKLAHWKDEFKSTLQHYWLGTKILMADVRISVRLLV /note-"Similar to Saccharomyces hypothetical protein P9642.2 (gb|U40828)." complement(join(42975. .43043,43213. .43339,43501. .43593, 43683. .43771,43856. .44002,44168. .44480,44564. .44922)) /gene="F5114.7" AAMYLKDTLGKEGIQELIQNLSKDKVFVVFRWQNTGGRLSEVSERD"
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gene

gene

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                                                                                                                                                 GGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTGTCGTG 425
TTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAAC 485
                                                                                                                                                                                                                                   466;
                                                                                                                GGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTGTCGTG 12594
                                                                                                                                                                                                                                      Conservative
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RIEGFGLARVIDSDDTNYKPGDIVSGIIGWEEYSLLRSSDNLQLRNIQLDDDIPLSYH
                                                                                                                                                                                                                                                                                                                                                                                  NVKIKGVLSLNSQLFHIAINRCRNIKIEDVRIIAPDESPNTDGIHIQLSTDIEVRNAS
IKTGDDCISIGPGTKNLMVDGITCGPGHGISIGSLAKSIEEQGVENVTVKNAVFVRTD
NGLRIKSWPRHSNGFVERVRFLGAIMVNVSYPILIDQNYCPGDSSCPSQESGIKINDV
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ESAKAFSDAWDAACGVEDSVVIYVPKGRYLVSGEVRFEGESCKSREITLRIDGTLIGP
QDYSLLGKKENWFSFSGVHNVTVLGGSFDAKGSTLWSCKANGYNCPEGATTLRINDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(53168. .53386,53596. .54114,54461. .54916))
/gene="F5I14.10"
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QKVEILKNELGYDEAFNYKEEADLDTALKRYFPBGIDIYFDNYGGSMLDAALLNMKVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Strong similarity
precursor (gb|U23053)."
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zeta-crystallin-like protein (gb|Z49268)."
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QYFREYYNGGWRSDHHSNWVSTSYSIL"
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CVEVGLPGLILLIFVTQYLPRPLKMKKGVMILDGSRCDRYGMILCIPLVWLFAQLLTS
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TLFQSFFGTRLDVIAVASYAYIIPITSIIYSTRETYYTDPFERFYRTMRSIQGALIIT
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IKKDDKLIKAEGVESLSEAELRQACRERGMLQLGSVEEMREQLVDWLDLSLNHSVPSS
                                                                                                                                                                                                                                                                                                                                                      IYSGIMGTSATEIAIKMDCSEKVPCTGIRMQAINLTSYGEAAKTSCTNVSGKQLGLVT
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/protein_id="AAB60909.1"
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17929. .48015.48122. .48218,48320. .48525,48704. .48799,
18884. .48959,49053. .49153,49242. .49418,49467. .49532
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100.0%;
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3. .52033,52078. .52294,52510. .52743))
                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                           Score 466; DB 8; L
Pred. No. 8.3e-100;
                                                                                                                                                                                                                             Mismatches
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGTAATAAAAATGAGAGGGGGAGAAAATGAGAGTGTTTTACTTATATAGTGTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2483 bp DNA linear PLN 22-DEC-Arabidopsis thaliana flowering locus T (FT) gene, complete cds. AF152096
                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                    Kardailsky, I. and Weigel, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activation tagging of the floral inducer FT Science 286 (5446), 1962-1965 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christensen, S.K., Nguyen, J.T., Chory, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kardailsky, I., Shukla, V.K., Ahn, J.H., Dagenais, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2483)
                /note="similar to hippocampal cholinergic neurostimulating
peptide (HCNP) precursor, phosphatidylethanolamine binding
protein (PEBP) and Raf kinase inhibitor protein;
                                                                          /gene="FT"
corresponds to
                                                                                                                                                                          /gene="FT"
                                                                                                                                                                                         join(1.
                                                                                                                                                                                                                                                                   /db_xref="taxon:3702"
/chromosome="I"
                                                                                                                    /gene="FT"
                                                                                                                                                      /product-"flowering
                                                                                                                                                                                                                                             /map="90 cM;
                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                 function="induces flowering"
                                                                                                                                                                                                             /gene="FT"
                                                                                                                                                                                                                                                               /chromosome=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:6117977
                                                                                                                                                                                          .264,1080. .1141,1855. .1895,2020.
                                                                                                     .1141,1855.
                                                                                                                                                          locus
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                                                                                                     .1895,2020.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2079 TTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 TTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGATAATTATTAATCTACATGAAATGAAGTGTTATATTAT 830
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                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (strain:Columbia) cDNA to mRNA. Arabidopsis thaliana (atrain:Columbia) cDNA to mRNA. Arabidopsis thaliana (atrain:Columbia) cDNA to mRNA. Pracheophyta; Tracheophyta; Embryophyta; Tracheophyta; Embryophyta; Embryophyta; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Araki, T. and Kobayashi, Y.
Direct Submission
Submitted (19-MAY-1999) Takashi Araki,
                                                                                                                                                  A pair of related genes with antagonistic flowering signals Science 286 (5446), 1960-1962 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSF
                                                                                                                                                                                                                                                     Kobayashi,Y., Kaya,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana TSF
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                                                                                            bases 1 to 799)
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/protein_id="AAF03936.1"
/protein_id="AAF03936.1"
/db_xref="GI:6117978"
/translat.ton="MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLR
PSQVQNKPRVEIGGEDLRNFYTLVMVDPDVPSPSNPHLREYLHWLVTDIPATTGTTFG
PSQVQNKPRVEIGGEDLRNVFILFRQLGRQTVVAPGWRQNFNTREFAEIYNLGLPVAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:4903015
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                                                                                                                                                                                                                                                     Goto, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 bp mRNA linear (TWIN SISTER OF FT) mRNA,
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                                                                                                                                                                                                                                                     Iwabuchi, M. and
      Grad.
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   of
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Science,
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                 CCGTGGCCGCAGTTTTCTACAATTGTCAGAGGGAGAGTGGCTGCGGAGGAAGAAGACTTT 588
                                                                                                                                                                                                                                                                       CAACTGGAĀCAACCTTTGGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAG
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                                                                                                     CAGGGTGGCGCCAGAACTTCAACACTCGCGAGTTTGCTGAGATCTACAATCTCGGCCTTC 528
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CTGTGGCTGCCTCTTACTTCAACTGCCAGAGGGAGAATGGCTGTGGGGGAAGAAGAACGT
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                                                                               {\tt CGGGGTGGCGCCAACAGTTCAACACTCGTGAGTTTGCTGAGATCTACAATCTTGGTCTTC}
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152 c
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772. 777
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/note="extensive homology with the similar to mammalian phophatidylethanolamine binding protein (PEBP) and hippocampal cholinergic
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32. .559
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/strain="Columbia"
/db_xref="taxon:3702"
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/db_xref="GI:4903016"
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Pred. No. 1.1e-81;
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ATGTCTATAAATATAAGAGACCCTCTTATAGTAAGCAGAGGTTGTTGGAGACGTTCTTGAT 122
                          CCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGGTGACTAATGGC 182
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-MAY-1999) Plant Biology Laboratory, Institute for Biological Studies, 10010 N. Torrey Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kardailsky,I., Shukla,V.K.,
Christensen,S.K., Nguyen,J.
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Haaksma, S., Shukla, V.K.,
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YFNCQRENGCGGRRT"
1 116 c 142 g 147 t
                                                                                                                                                                                                                                                                                                                   /note-"flowering locus T (FT) homolog; similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PE and Raf kinase inhibitor protein"
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PSQVLNKPIVEIGGDDFRNFYTLVMVDPDVPSPSNPHQREYLHWLVTDIPATTGNAFG
                                                                                                                                                                                                                                                              /product="twin sister of FT"
/protein_id="AAF03937.1"
/db_xref="GI:6117980"
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/chromosome="IV"
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Nguyen, J.T., Chory, J.,
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            Local
                                                                                                                    PI TAKASHI ARAKI,KYOJI KOBAYASHI,KENICHI OGAWA,MAKOTO SHIRAI PC.
A01H1/00,A01H5/00,C12N5/10,C12N15/09//(C12N5/10,C12R1:91), PC
(C12N15/09,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91), PC
(C12N15/00,C12R1:91)
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                                                                                                                                                                                                                                                                               TORAY IND INC
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                                                                                         /organism='Arabidopsis'
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Score 374.4; DB 6;
Pred. No. 4.7e-78;
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                                                                                                                                                                                                                                                                                                                                                           Citrus unshiu (strain:Miyagawa-wase satsuma mandarin) stage juice sac and pulp segment cDNA to mRNA. Citrus unshiu
                                                                                                                                                           Submitted (17-MAY-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu; Okitsu, Shimizu, Shizuoka 424-0292, Japan (E-mail:om9330@okt.affrc.go.jp, Tel:81-543-69-7108, Fax:81-543-69-2115)
                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                     2 (bases 1 to 745)
Omura, M., Kobayashi, Y. and Araki, T.
                                                                                                                                                                                                                                                20050958
                                                                                                                                                                                                                                                                       A pair of related genes with antagonistic roles flowering signals
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 /gene="CiFT"
/note="extensive
                                                             /dev_stage="developing stage juice sac and
/note="partial sequence (pcMFRI727.131) is
Accession Number C24153"
                                                                                                                                              Location/Qualifiers
                                                                                               /strain="Miyagawa-wase satsuma
/db_xref="taxon:55188"
                                   /gene="CifT"
                                                                                                                      organism="Citrus unshiu"
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Floral development genes Patent: WO 0244390-A 11 (E. I. du Pont de Nemours
                                                                Cahoon, E.B.,
                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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/db_xref="G1:4903139"
/db_xref="G1:4903139"
/translation="MSSRERDPLIVGRVVGDVLDNETRTIPMRITYSNKDVNNGRELK
/translation="MSSRERDPLIVGRVVGDVLDNETRTIPMRITYSNKDVNNGRELK
PSEVLMQPRAEIGGDDLTRTYTLVMVDPDAPSPSDPSLREYLHMIVTDIPATTGASFG
QEIVNYESPRPTMGIHRFVFVLFRQLGRQTVYAPGWRQNFSTRDFAELYNLGPPVAAV
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Cramaronhyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
2 (bases 1 to 847)
Yano, M. and Kojima, S.
Direct Submission
Submitted (33-DEC-2000) Masahiro Yano, National Institute of Agrobiological Resources, Department of Molecular Genetics; Kannondai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                             Kojima,
Hd3a, č
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Oryza sativa (indica cultivar-group)
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/db_xref="GI:14517622"
/translation="MACSGRDPLVVGRVVGDVLDAFVRSTNLKVTYGSKTVSNGCE/translation="MACSGRDPLTVGRVVGDVLDAFVRSTNLKVTYGSKTVSNGCELXPSMVTHQPRVEVGROMMRTFYTLVMVDPDAPSPSDPNLREYLHWLVTDIPGTTAASFGQEVMCYESPRPTMGIHRLVFVLFQQLGRQTVYAPGWRQNFNTKDFAELYNLGSPVAAVYFNCQREAGSGGRRVYN"
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/cultivar="Kasalath"
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Bovine embryonic	ABN73981	24	910	5.6	48	5
. Bovine embryonic g	ABN73980	24	910	٠	48	44
Human colon cancer	AAH34361	22	S		48	3
Cu	AAF16381	21	551		48	42
Bovine embryonic g	ABN74051	24	.939	5.6	48.2	41
Novel cDNA encodir	AAS28106	22	367		48.2	0
DNA transcription	ABK28390	24	7589	5.7	48.4	39
	AAK62481	22	475	5.7		38
ovarian a	ABQ54500	24	427	5.7	48.6	37
Human secreted pro	AAD34120	24	2637	5.7	•	36
Bovine embryonic g	ABN742.79	24	956	5.7	48.8	35
Proliferative glom	ABA77106	22	1012		49	34
Human angiogenesis	ABQ67094	24	83391		49.2	ω
Proliferative glon	ABA77091	22	978		49.2	32
Bovine embryonic g	ABN74030	24	925		•	3
	ABK41982	23	503		49.2	30
Human immune/haema	AAK60828	22	649		50	29
Human metastasis a	ABL34609	24	18585		50.2	28
Human colon cancer	AAH35052	22	557		50.2	27
Bovine embryonic g	ABN74181	24	988	6.0	51	26
Bovine embryonic g	ABN73995	24	970		51.2	25
Porcine complement	AAZ30973	20	1637		51.8	24
Spinach lycopene e	AAD17465	22	2426		52.8	23
Human ovarian anti	ABQ55599	24	567		55.6	22
Strawberry floweri	AAC90667	22	4952		63	21
OV-16 antigen. On	AAQ14832	12	822	8.4	71.8	20
Arabidopsis termin	AAT60142	18	1430		80	19
Ħ	AAC90666	22	3696		82.6	18
	w	18	929	ω	116	17
	AAV66749	19	4512	7.	145.8	16
_	AAC90668	22	519	8	161.2	15
	ABK82094	24	787	0	175	14
ncoding	ABK82122	24	1225	0	176	13
	209	24	792	20.6	176	12
ncoding	N)	24	792	0	176	F
Novel floral meris	ABK82093	24	762	20.6	176	0

ALIGNMENTS

ВP

Flowering locus T gene; FT; flowering time; modulator; early flowering; antibody; cellular binding protein; crop; ss. Weigel D; (SALK) SALK INST BIOLOGICAL STUDIES Arabidopsis thaliana. Flowering locus T (FT) gene (first entry) 98US-0060726 99WO-US08151 Location/Qualifiers 63..590 /*tag= a /product= FT /note= "Flowering locus

Result No.

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Matches 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the flowering locus T (FT) gene of Arabidopsis thaliana FT regulates flowering in plants by modulating flowering time. For regulates flowering in plants by modulating flowering time. Overexpression of FT results in early flowering, while loss of function mutations or antisense directed to FT causes late flowering. The FT polypeptide has a molecular weight of approximately 20kD, and is located to become 1 management of approximately 20kD, and is located to become 1 management of approximately 20kD, and is located to become 1 management of approximately 20kD, and is located to be compared to the province of the second of th
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TTTAATAACCATTTTATGATACGAGTAACGAACGGTGATGATGCCTATAGTAGTTCAATA
                                                                  CCTTTATAACCAATTGATATTGCATACTCTGATGAGATTTATGCATCTATAGTATTTTAA 660
                                                                                                                                AGAACTTCAACACTCGCGAGTTTGCTGAGATCTACAATCTCGGCCTTCCCGTGGCCGCAG
                                                                                                                                                                                                                                                                                                                 CCTTTGGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTG
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DB; AAY49098.
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856; Conserv
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TCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCAGCACGAGGTTTGTTCAAGATCAA

Matches Query Match Best Local :

Local Similarity

100.0%; ilarity 100.0%; Conservative

0

Score 856; DB 20; Pred. No. 3.8e-190;); Mismatches 0;

Length Indels

0;

Gaps 60

0

Sequence

856

BP;

249

A; 194 C;

150 <u>ດ</u>

263 T; 0 other;

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RESULT 2
AAZ284491/c
ID AAZ284
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                                                 This is the flowering locus T (FT) gene antisense polynucleotide construct. This sequence is used in the production of the antisense construct of the invention pSKIO60. FT regulates flowering in plants by commodulating flowering. time. Overexpression of FT results in early commodulating flowering. Time for polypeptide has a molecular weight of conservation to modulate flowering the FT polypeptide has a molecular weight of comproximately 20kb, and is located on chromosome 1. The FT polypeptide is cused in the invention to modulate flowering time in many mono and control to the composition of the polypeptide, and as a source of antisense, ribozyme or triplex forming sequences. The FT polypeptide can also be cused to raise antibodies and to screen for modulators or cellular binding proteins. The methods of the invention allow for the production of crops at any time of year.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flowering
antibody;
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ing protein; crop; antisense construct; ss.
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              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                              Arabidopsis
                                                                                                             17-OCT-2000
                                                                                                                                            AAC34682;
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AAAAAAAAAAAACTCGAG 1
                                                                                                                                                                                                                                                                                                                ACCTCAGGAACTTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACC
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                                      Similarity 99.193; Conservative
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(first entry) thaliana DNA fragment SEQ ID NO: 57192. thaliana DNA fragment SEQ ID NO: 57192. n assay; genetic mapping; gene expression control; tification; signal transduction pathway; thway; promoter; termination sequence; ss. thaliana. 2000EP-0301439. 99US-0121825. 99US-0121825. 99US-01235788. 99US-01235788. 99US-01235788. 99US-012462. 99US-012462. 99US-0130409. 99US-0130409. 99US-0130449. 99US-0131449. 99US-0131449. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0134218. 99US-0134370. 99US-0134370. 99US-01343768.	GCAGGAATTCATCGTGTGTGTTATATATGTTTCGACAGCTTGGGAGGCAAACAGTGTAT 484 GCACCAGGGTGGCGCAGAACTTCAACACTCGCGAGTTTGGTAGAATCTACAATCTCGGC 524
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                                                                     DNA;
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                           nucleotide sequence
             Cruciferae; plant; control; flowering;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
                                                                                                                                                                                                                                                                                                                                                                                  2000-425906/37.
DB; AAB12459.
                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTCTATAAATATAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGAT 122
                                                                                                     GTGTTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAG
                                                                                                                                                       CTCAGGAACTTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACCCT
TTCTACAATTGTCAGAGGGAGAGTGGCTGCGGAGGAAGAAGACTTTAG
                                                                                                                                                                                                                                                                                                                              TTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGAC
                                                                                                                                                                                                                                                                                                                                                                       CCGTTTAATAGATCAATCACTCTAAAAGGTTACTTATGGCCAAAGAGAGGTGACTAATGGC
                                                   ACTTCAACACTCGCGAGTTTGCTGAGATCTACAATCTCGGCCTTCCCGTGGCCGAGTT
                                                                             AACTTCAACACTCGCGAGTTTGCTGAGATCTACAATCTCGGCCTTCCCGTGGCCGCAGTT
                                                                                                                                                                                                                                                                CTCAGGAACTTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to accelerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.7%; Silarity 100.0%; Conservative 0;
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Pred. No. 1.1e-113;
0; Mismatches 0;
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RESULT 6

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06-MAY-1999,
07-MAY-1999,
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21-MAY-1999,
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ
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990S-0131449
990S-0132048
990S-0132048
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990S-0132487
990S-0134287
990S-0134256
990S-0134219
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99US-0130449.
99US-0130510.
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99US-0128234.
99US-0128714.
99US-0129845.
99US-0134941

99US-0135124

99US-0135629

99US-0136782

99US-0136782

99US-0136782

99US-0137528

99US-0137528

99US-0137502

99US-0137502

99US-0138640

99US-0138640

99US-0138647

99US-0138647

99US-0139452

99US-0139452

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99US-0123548
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Best Local Similarity
Matches 434; Conser
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13 - SEP - 1999
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                                          ATGTCTATAAATATAAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGAT
           TTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGAC
 TTGGATCTAAGGCCTTCTCAAGTTCTGAACAAACCAATAGTGGAGAATTGGAGGAGACGAC
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-1999;
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nilarity 82.2%;
Conservative
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990S-0149929
990S-0149930
990S-0150866
990S-0151066
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990S-0153786
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                                                                                                                                     Score 377.6; DB 21
Pred. No. 1.2e-78;
0; Mismatches 94;
                                                                                                                                                           21;
                                                                                                                                      Indels
                                                                                                                                                            Length
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                                                                                                                                      Gaps
180
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18-JUN-1999
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990S-0139459
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990S-0142087
990S-01422055
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990S-0147204
990S-0147303
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990S-0148319
990S-0148684
990S-0149723

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 Query Match
Best Local Similarity
Matches 432; Conserv
                                                                           the present invention describes a method to accelerate plant generation and generation accelerated plants. The method uses a controlling gene functioning in the downstream of a gene under the control of solar radiation to accelerate plant generation using a gene functioning to accelerate the flowering time regardless of solar radiation. The method can control flowering time to a desired period by shortening the juvenile stage. The present sequence represents a specifically claimed Arabidopsis nucleotide sequence, which is used in the exemplification
                                                                                                                                                                                   Claim 5; Page 5; 6pp; Japanese
                                                                                                                                                                                                                A method to accelerate plant generation and plants -
                                                                                                                                                                                                                                              WPI; 2000-425906/37
                                                                                                                                                                                                                                                                                           11-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA60684;
                                               Sequence
                                                                                                                                                                                                                                                                                                                                          23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                      present invention
                                               528
  Conservative
                                            ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                  98JP-0320219.
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            43.7%;
81.8%;
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                                             117
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 Score 374.4; DB 21.
Pred. No. 6.9e-78;
0; Mismatches 96;
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                                             T; 0 other;
                     DB 21; Length
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                                                                P-PSDB;
                                                                                              Oeller P,
                                                                                                                                     24-MAY-2000;
                                                                                                                                                25-MAY-1999;
                                                                                                                                                                    24-MAY-2000;
                                                                                                                                                                                          30-NOV-2000
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                                                                                                                                                                                                                                  Fragaria vesca
                                                                                                                                                                                                                                                                                    Strawberry flowering regulation protein coding sequence
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Novel nucleic acid involved in controlling plant flowering processes useful for generating transgenic plants, in particular strawberry plants having altered flowering behavior such as early, delayed or day-neutral flowering

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RRSULT 9
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                                                      mutation
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                                                                                                                                                                                                                      transgenic
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                                                                                                                                                                         thaliana var. Columbia
                                                                                                                                                                                                                                                                                            terminal flower1 (tfl1) cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antirrhinum majus centroradialis gene and Arabidopsis homologue, Tfll - control switching of apical meristem to floral fate, usef in plant hybridisation and in control of growing season
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 668 BP; 195 A; 135 C; 147 G; 191 T; 0 other;
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P-PSDB; AAW13945.
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GTCGTGTTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGC---ACCAGGGTGG
                                                                                                      CCTCACCTCCGAGAATATCTCCATTGGTTGGTGACTGATATCCCTTGCTACAACTGGAACA
                                                                                                                                                           GACCTCAGGAACTTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAAC
                                                                                                                                                                                                                      GGCTTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAA
                                                                                                                                                                                                                                                                                GATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGGTGACTAAT 179
                                                                                                                                                                                                                                                                                                                         AATATGGGAACTAGAGTGATAGAGCCATTGATAATGGGGAGAGTGGTAGGAGATGTTCTT
                            ACGTTTGGCAAAGAGGTGGTGAGCTATGAATTGCCAAGGCCAAGCATAGGGATACATAGG
                                                      ACCTTTGGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGT
                                                                                     CCCTTTCTAAAAGAACACCTGCACTGGATCGTTACAAACATTCCCGGCACAACAGATGCT
                                                                                                                                               GATCTCAGATCCTTCTTCACTTTGGTGATGATAGACCCAGATGTTCCAGGTCCTAGTGAC
                                                                                                                                                                                                        GGCCATGAGCTCTTTCCTTCTTGTTTCCTCCAAGCCTAGGGTTGAGATCCATGGTGGT
                                                                                                                                                                                                                                                                GATTTCTTCACTCCAACAACTAAGATGAATGTTAGTTATAACAAGAAGCAAGTCTCCAAT
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The invention describes a substantially purified or isolated polypeptide CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. CC and HB-like proteins, or their functionally active fragments or variants. CC architecture and/or sing (II), is useful for modifying plant life cycles architecture and/or flowering processes, flowering and/or plant. The CC which involves introducing (II), (III) or (IV) into the plant. The CC individual or simultaneous enhancement or downregulation of MADS-box CC gene activities may alter flower, embryo and seed development, e.g., CC enhance or inhibit embryo differentiation and growth or alter flower CC organ identity through conversion of one floral organ in another. CC Manipulation of CEN or HB activity in plants alters the control of phase CC change, flowering time and the number of leaves made before flowering. CC Manipulation of AP2 activity in plants alters flower organ identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass fescue species, useful for controlling plant life cycles and/or growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein; HB-like protein; plant growth; plant architecture; inflorescence development; flower development; embryo development; seed development; flower organ identity; phase change; male sterility; hybrid seed production; herbage quality; early maturing crop; blomass increase; blocking flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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KW hyl)

DNA encoding novel floral meristem identity protein LpCENa

27-AUG-2002

(first entry)

ABK82091;

ABK82091 standard;

cDNA; 792

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase blomass production; increasing branching to enhanced business in fruit trees; altering plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This sequence represents a contig polynucleotide novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 762 BP;
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                                                                                 CAGTTTGCTGTGGATAATGATCTTGGCCTCCCTGTGGCTGCTGTTTACTTCAATTGTCAG
                                                                                                                        GAGTTTGCTGAGATCTACAATCTCGGCCTTCCCGTGGCCGCAGTTTTCTACAATTGTCAG
                                                                                                                                                                  AAGCAGAAGCGAAGGCAGACTGTATCTGTGCCTTCCTTCAGGGATCATTTCAACACCCGC
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AGAGAGACTGCCAGGAGGCGCTGAAAATCGAGTTCTT
                                     AGGGAGAGTGGCTGCGGAGGAAGAAGACTTTAGATGGCTT 597
                                                                                                                                                                                                            CGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAACTTCAACACTCGC
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Pred. No. 1.4e-31;
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                                                                                                                                                                                                                                                                                               The invention describes a substantially purified or isolated polypeptide CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) CC and HB-like proteins, or their functionally active fragments or variants: CC vector (IV) comprising (II), is useful for modifying plant life cycles architecture and/or flower and/or inflorescence development in a plant, CC which involves introducing (II), or (III) or (IV) into the plant. The CC individual or simultaneous enhancement or downregulation of MADS-box CC gene activities may alter flower, embryo and seed development, e.g., CC enhance or inhibit embryo differentiation and growth or alter flower CC organ identity through conversion of one floral organ in another.

CC Manipulation of CEN or HB activity in plants alters the control of phase C change, flowering time and the number of leaves made before flowering. CC through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of CC flowering pant architecture has a wide range of applications such as: CC inducing male sterility for hybrid seed production; changing flowering in CC increasing herbage quality; altering flowering time allowing early conversion branched business in fruit trees; altering plant CC increase for allergenic pollen. This sequence encodes a novel floral converses the stature; and in blocking flowering and reducting CC through conversion involved in floral development and a potential CC through in the floral involved in floral development and a potential CC through in the floral involved in floral development and a potential CC through in the floral involved in floral development and a potential CC through in the floral involved in floral development and a potential CC through the floral involved in floral development and a potential CC through the floral inv
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Best Local
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 30; 290pp; English
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                                                                                                                                                                GACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGATCCGTTTAATAGATCAATC 140
TCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGACCTCAGGAACTTCTAT
                                        AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCA
                                                                                 ACTCTAAAGGTTACTTATGGCCAAAGAGAGGTGAC---TAATGGCTTGGATCTAAGGCCT 197
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Pred. No. 1.4e-31;
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                                                                        New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass fescue species, useful for controlling plant life cycles and/or growt
                                                                                                                                                       Spangenberg G,
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The invention describes a substantially purified or (I) from a ryegrass (Lolium $\operatorname{sp.}$) or fescue (Festuca

sp.) species, such a

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growth

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Claim 4; Fig 32; 290pp; English

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AGAGAGACTGCCAGGAGGCGCTGAAAATCGAGTTCTT
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Pred. No. 1.4e-31;
0; Mismatches 205;
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New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass fescue species, useful for controlling plant life cycles and/or growt phases

Claim 4; Fig 49; 290pp; English.

The invention describes a substantially purified or isolated polypeptide C(I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APETRALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) CC and HB-like proteins, or their functionally active fragments or variants. CC vector (IV) comprising (II), a construct (III) comprising (II), or a construct (III) comprising (III), or a construct (III) comprising comprising (III), or a construct (III) comprising companity (III), or a construct the plant. The construct (III) comprising construction (III) comprising comprising construction (III) comprising construction (III) comprising construction (III) comp meristem identity protein involved target for manipulating plant life in floral cycles. development potential

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                                17-OCT-2001;
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                                                                                                                                                                                                                         Novel floral meristem identity gene LpCENa contig #3.
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312; Conser
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Query Match Best Local s Matches

Similarity

20.4%;

Conservative

0

Score 175; DB 24; Pred. No. 2.4e-31; 0; Mismatches 206;

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ACTCTAAAGGTTACTTATGGCCAAAGAGAGGTGAC---TAATGGCTTGGATCTAAGGCCT 197

AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCA

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437

CTCCATTGGTTGGTGACTGATATCCCTGCTACAACTGGAACAACCTTTGGCAATGAGATT

286 258 226 198 166

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flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; increasing branching to engage the plant stature; and in blocking flowering and reducing release for allergenic pollen. This sequence represents a contig polynucleotide novel floral meristem identity protein involved in floral polynucleotide novel floral meristem identity protein involved in floral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and HB-like proteins, or their functionally active fragments or variants. Function of the proteins of their functionally active fragments or variants. The protein of the p
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                                                                                 development and a potential target for manipulating plant life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-liproteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a substantially purified or isolated polypeptide
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                                                                                                                       Matches
                                                                                                                                                    Query Match
                                                                                                                                                                                                         The present invention provides the nucleic acid and protein sequences of a number of proteins from the strawberry which are involved in the regulation of flowering. These were identified using primers based on the homologous sequences from A. thaliana, B. napus and R. sativus. They can be used in the production of transgenic field crops whose flowering is regulated and the time of fruiting and harvesting can be manipulated.
                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid involved in controlling plant flowering processes useful for generating transgenic plants, in particular strawberry plants having altered flowering behavior such as early, delayed or day-neutral flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oeller P, Gutterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strawberry; flowering regulation; harvesting; fruit production; ss.
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                                                                                                                                                                               Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                      Claim 23; Page 94-95; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB50271.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-025165/03
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Local Similarity 57.9%;
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CCCCACTACAAAAATGATTGTCTCTTACAACAGCAAGCTCGTCTGCAATGGACATGAGCT
                                                                          AAATATAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGATCCGTTTAA 130
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ALIGNMENTS

FEATURES SOURCE	ORGANISM ORGANISM REFERENCE AUTHORS TITLE TOURNAL MEDLINE COMMENT	AV563203/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS
The First Laboratory for Plant Gene Research Kazusa 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers 1. 518 /organism="Arabidopsis thaliana" /strain="Columbia"	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 518) Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries DNA Res. 7, 175-180 (2000) 20363093 Contact: Erika Asamizu	AV563203 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana columbia Arabidopsis av563203 Av56320 Av563203 Av56320 Av5620 Av562

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                                                      Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized an size-selected cDNA libraries
                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
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Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Arakawa,T., Shibata,K., Shinagawa,A., Muram
                                                                                          EST
                                                                                                   AV788551
AV788551.1
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Location/Qualifiers
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/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ169b07F"
                                                                                                    GI:19807341
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                    Satou, M.,
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            Ishii,Y.,
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                                                                                                                                                                                AGAGGGGAAGAAATGAGAGTGTTTTACTTATATAGTGTGTGATGCGATAATTATATTA
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                                                                                                                                                                                                                                                                                                                                                              AGAGTGGCTGCGGAGGAAGAAGACTTTAGATGGCTTCTTCCTTTATAACCAATTGATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423;
    WHE0855_C01_E012S Wheat 20-45 DAP spike cDNA Library aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length c
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/db_xref="taxon:3702"
/clone="RAFL06-80-B19"
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GTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTGTCGTGTTTATATTTGTTT 437
                                                                          CTCCATTGGTTGGTGACTATATCCCTGCTACAACTGGAACAACCTTTGGCAATGAGATT 377
                                              CTCCACTGGCTTGTGACAGATATCCCCGGTACAACTGGTGCATCCTTCGGGCAGGAGGTG 384
                                                                                                       ACACTCGTGATGGTAGACCCAGATGCTCCAAGTCCAAGCGATCCCAACCTTAGGGAGTAT 324
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VERSION
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ACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACCCTCACCTCCGAGAATAT 317
                                                                           TCCATGGTCGCCCAGCAGCCCAGGGTTGAGGTGGGCCGGCAATGAGATGAGGACCTTCTAC 264
                                                                                                                                                                                         ACCAACCTCAGGGTGACCTTCGGGAACAGGACCGTGTCCAACGGCTGCGAGCTCAAGCCG
                                                                                                                                                                                                                                             ATCACTCTAAAGGTTACTTATGGCCAAAGAGAGGTGACTAATGGCTTGGATCTAAGGCCT 197
                                                                                                                                                                                                                                                                                                    AGAGACCCGCTGGTGGTTGGCAGGGTTGTGGGGGGACGTGCTGGACCCCTTCATCCGGACC 144
                                                                                                                                  TCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGACCTCAGGAACTTCTAT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture R
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., F., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed port. genomes - 20-45 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: oandersn@pw.usda.gov
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
Sequence have been in the sequence less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-TARP XR, excised phagemid;
/note="Vector: Lambda Uni-TARP XR, excised prown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared, a
cDNA library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
(Choi, Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Spike and seed"
/dev_stage="nhd",'t
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/db_xref="taxon:4565"
/clone="WHE0855_C01_E01"
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68.9%;
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Vinifera cDNA clone RT071D11 3', mRNA sequence.
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Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
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/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Ec
/note="Organ: Lambda IP Content of Stage II Site_1: Ec
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/dev_stage="ripening stage"
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/clone="RT071D11"
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TTCAATATATAAGTGTGTAATAAAAA
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AV560420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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AV560420
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1 (bases 1 to 206)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
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/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
//orite="Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ134d05F"
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CAGCAGCTGGGGCGCCAGACCGTGTACGCCCCGGGCTGGCGCCAGAACTTCAACACCAGG
                 CGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAACTTCAACACTCGC
                                                                      ATCTGCTACGAGAGCCCTCGGCCGACCATGGGGGATCCACCGCTTCGTGCTGCTGCTGTTC
                                                                                                                                             CTACACTGGCTGACGGATATTCCGGGAACTACTGGGGCAGCATTTGGGCAAGAGGTG
                                                                                                                                                                  CTCCATTGGTTGGTGACTGATATCCCTGCTACAACTGGAACAACCTTTGGCAATGAGATT
                                                                                                                                                                                                                                                                                                                               TCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGACCTCAGGAACTTCTAT 257
                                                                                                                                                                                                                                                                                                                                                                   ACCAACCTCAGGGTCAGCTACGGGGCCCAGGACCGTGTCCAACGGCTGCGAGCTCAAGCCG
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                                                                                                           GTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTGTCGTGTTTATATTGTTT
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S. Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/db_xref="MaizeDB:632948"
/db_xref="taxon:4577"
/clone="CL846_1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHE0963_B10_C19ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0963_B10_C19, mRNA sequence.
BE498304
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                                                                                                                                                     /lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhOI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside, Plasmid DNA
                                                                                       preparations and DNA sequencing were Anderson lab (all other authors)."
148 c 160 g 98 t
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/tissue_type="Spike before anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Query Match Best Local Similarity

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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J.
Anderson,O.D., Chao,S., Lazo,G.R., Miller
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF483056
491 bp mRNA linear EST WHE2314_C03_E06ZS Wheat pre-anthesis spike cDNA library aestivum cDNA clone WHE2314_C03_E06, mRNA sequence.
BF483056
                                                                                                                                                                           Email: oandersnepw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                               US Department of Agriculture, Agriculture Research West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
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EST.
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                                          /clone_lib="Wheat pre-anthesis spike
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
                                                                                                    /cultivar="Chinese Spring"
/db_xref="taxon:4565"
 /note="Vector: Lambda Uni-ZAP
Site_1: EcoRI; Site_2: XhoI; F
                                                                                        /clone="WHE2314_C03_E06"
                                                                                                                                                                Location/Qualifiers
                                /lab_host="E. coli
                                                                                                                                   /organism="Triticum aestivum|
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Local Similarity
nes 276; Conserv
CAGCAGCTCGGCCGCATACCGTGTCCGCTCCCGGGTGGCGCCAGAACT
                                           CGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAGAACT 486
                                                                                                                          GTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTGTCGTGTTTATATTGTTT 437
                                                                                                                                                                                            CTCCACTGGCTTGTGACAGATATCCCCCGGTACAACTGGTGCATCCTTCNGGCAGGAGGTG
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Pred. No. 1.6e-24;
D; Mismatches 133;
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AV937451 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bahlln08 5', mRNA sequence.

AV937451 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002) Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; 1111 Yata, Mishima,
Tel: 81-559-81-6856 Contact: Tadasu Shin-i AV937451.1 GI:18233248 Spermatophyta; Magnoliophyta; Fax: 81-559-81-6855 Triticeae; (bases 1 to 542) tshini@genes.nig.ac.jp Location/Qualifiers /organism="Hordeum vulgare /strain="H602" Hordeum. Liliopsida; NIG subsp. spontaneum" and Japan Embryophyta; Tracheophyta; a; Poales; Poaceae; Pooidea Okayama 18-JAN-2002 Pooideae

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RESULT 11
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Contact: Michael G. Hahn
Complex Carbohydrate Research
University of Georgia
                                                   Hahn, M.G., Ojanen-Reuhs, T., Samac, D., 7
Utterback, T., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula
oligogalacturonides of DP 6-20
                                                                                                                                 Medicago truncatula

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/clone="bahlin08"
/clone="bahlin08"
/clone=lib="K. Sato unpublished cDNA library, strain adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/dev_stage="adult, heading stage"
150 c 146 g 124 t 2 others
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available at: www.medicago.org
seq primer: SKmod (CTA 9AA CTA
Location/Qualifiers
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/dev_stage="24 hours after treatment in
with 0.5 mg/ml oligogalacturonides (DP of
presence of 100 ug/ml Gentamicin"
/lab_host="XIOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/cultivar="A17"
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                                                                                                                                                                                                                                               170 GGTGACTAATGGCTTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                            53 AAGATCAAAGATGTCTATAAATATAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGA 112
AACTGATGCTTCTTTTGGAAAAGAGATAGTGAGCTACGATAGTCCAAAACCAGTGATCGG
                                                                                                                                                                                                               AGTGTTTAATGGTCACGAACTCATGCCTCCTATCATTGCTTCTAAGCCTCGTGTGGAGAT
                                 AACTGGAACAACCTTTGGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGG
                                                                                       TGGTGGTGAAGACATGAGATCTGCTTATACACTCATCATGACTGATCCAGATGTTCCAGG
                                                                                                                                                                                                                                                                                                                       CGTTCTTGATCCGTTTAATAGATCAATCACTCTAAAGGTTA---CTTATGGCCAAAGAGA 169
                                                                      TCCTAGTGATCCTTACTTAAGGGAACACCTCCACTGGATTGTGACAGATATTCCTGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone info: please contact Research Genetics, Division tel_1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@resgen.com
For clone info: please
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots weilsolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

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/tissue_type="roots"
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/clone="cPRO30M16"
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/cultivar="Kennebec"
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                                               GCTCCAAGCCCAAGTCACCCATCACTAAGGGAGTACTTGCACTGGATGGTGTCAGACATC
                                                                             GTTGATTTCGGTGGCAGTGACATGAGAGTTCTACACACCCTGATATTGGTGGATCCAGAC
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1111 Yata, Mishima, Shizuoka 4
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Akashinriki vegetative stage leaves"
/tissue_type="leaves"
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                                                                                                                                               ACGTTCTTGATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGGG
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                                                                                                                            ATGTGCTTGATCCATTTACATCAACCGTTCCATTAAGGATAGCCTACAACAATAGGCTAG
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GTGGCAGTGACATGAGAGTTCTACACACCCTGATATTGGTGGATCCAGACGCTCCAAGCC
                                                                                              TGACTAATGGCTTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTG
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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1111 Yata, Mishima, Shizuoka 411-8540,
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Barley EST sequencing project in NIG and Okayama Univ
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Location/Qualifiers
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Akashinriki vegetative stage leaves"
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/cultivar="Akashinriki"
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BJ315664 Y. Ogihara unpublished cDNA library, WY
aestivum cDNA clone whyf19i17 5', mRNA sequence.
BJ315664
BJ315664.1 GI:20121218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-8856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in Triticum aestivum Unpublished (2002)
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Ogihara, Y. and Murai, K.
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        Conservative
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Location/Qualifiers
                                                                                                        Plasmid DNA preparations and DNA performed in the OD Anderson lab 151 c 143 g 147 t
                                                                                                                                                              library was made, and the cDNA clones were in vivo excised to give paluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chi, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
                                                                                                                                                                                                                                          in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the samples, polyA was purified from the pooled RNA, a cl
                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: ECORI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Y. Ogihara unpublished cDNA library, Wh_yf"
/tissue_type="spikelet at early flowering"
/dev_stage="Feekes' scale 6"
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Search completed: May 2, 2003, 11:50:30 Job time: 1791.5 secs

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7, Appli 54, Appl 14, Appl 12, Appli 12, Appli 12, Appli 14, Appl 14, Appl 14, Appl 14, Appl 14, Appl 14, Appli 14, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19,

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greater than or equal to the scores derived by analysis of the total
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Best Local Similarity
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APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS
TITLE OF INVENTION: MODIFIED PLANTS
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CURRENT APPLICATION NUMBER: US/09/060,726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
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                                              CCTTTGGCAATGAGATTGTGTGTTACGAAAATCCAAGTCCCACTGCAGGAATTCATCGTG
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US-08-818-111-14
US-09-056-556-14
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LENGTH: 855
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CURRENT APPLICATION NUMBER: US/09/060,726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
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APPLICANT: Salk Institute
TITLE OF INVENTION: PLOWERING LOCUS
TITLE OF INVENTION: MODIFIED PLANTS
FILE REFERENCE: SALKINS.026A
                                                                                                                                                LENGTH: 855
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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RESULT 3
US-07-644-372-1
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                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lazzeri, Mario E.
APPLICANT: Nutman, Thomas B.
APPLICANT: Weiss, Niklaus
APPLICANT: Weiss, Niklaus
TITLE OF INVENTION: A DNA SEGMENT ENCODING
TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                         ADDRESSEE: CUSHMA
STREET: 1615 L. S
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAAAAACTCGAG 856
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   PatentIn Release #1.0,
   Version
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CURRENT APPLICATION DATA:

US/07/644,372

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US-08-467-948A-3/C
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Datent No. 5998164
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Best Local Similarity
Matches 217; Conserv
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                                                       APPLICANT: GUNTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
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                                     CORRESPONDENCE ADDRESS:
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LOCATION:
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                       ADDRESSEE:
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1100 NEW YORK AVE.,
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NI, JIAN
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Pred. No. 5.8e-10;
GOLDSTEIN & FOX P.L.L.C. NW, SUITE 600
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
              SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
                                                                                                                    COUNTRY:
                                                                                                                                         CITY: WASHINGTON
STATE: DC
                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 30-MAR-1995
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5. 6090575
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l Similarity 90.9%;
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BULT, CAROL J.
SUTTON III, GRANGER G.
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US/08/467,947A
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                              VERSION #1.30
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; NAME/KEY:
; LOCATION:
US-08-467-947A-3
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                TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                              REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
SEQUENCE CHARACTERISTICS:
                                                                                                 FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,0
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 07-JUI
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                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                   80203
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                               USA
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90.9%;
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Pred. No.
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AND USES THEREOF
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; NAME/KEY: CDS
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US-08-482-130C-60
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Best Local Similarity
           Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: L.
CITY: Denver
CITY: Colorado
"NTE: CISA
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/482,130C FILING DATE: 07-JUN-1995
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Conservative
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73.2%;
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73.2%;
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FLEA PROTEASE PROTEINS, NUCLEIC ACID
MOLECULES, AND USES THEREOF
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Pred. No. 0.0015;
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           Score 46.8; DB 2;
Pred. No. 0.0015;
 Mismatches
                         Length 234;
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Indels
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Gaps
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RESULT 9
US-08-906-769-60
; Sequence 60, Application US/08906769
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                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NÚMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                             108
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                                                                                          61 AGATGTCTATAAATATAAGAGA 82
                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/484,211C
FILING DATE: 07-JUN-1995
                                                                                                                                                                                          Local Similarity 73.2 les 60; Conservative
                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
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                                                                           GCGCGTCTCATCTTACAAGATA 129
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                                                                                                                                  INFORMATION:
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1700 Lincoln Street, Suite 3500
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Pred. No. 0.0015;
0; Mismatches 2
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                                                                          GENERAL INFORMATION:
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RESULT 10
US-08-906-616-60
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Sequence 60,
Patent No. 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-02
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Silver, Gary TITLE OF INVENTION: FLE TITLE OF INVENTION: MOL
                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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CITY: [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Connell, Gary J. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                    61 AGATGTCTATAAATATAAGAGA 82
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                         GCGCGTCTCATCTTACAAGATA 129
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0, Application US/08906616
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1..234
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Pred. No. 0.0015;
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Wu Hunter, Shirley

Grieve, Rushlow,

Robert B.

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US-08-906-616-60
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Best Local Similarity
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                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 234 base pairs
                                                                       TITLE OF INVENTION:
                                                                                                                      \PPLICANT
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 base pairs
                                  Stiegler, Gary
Stiegler, Gary
VENTION: USE OF PROTEASE INHIBITORS AND
VENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
VENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
                                                                                                                                                                             Rushlow, Ker...
The shirley Wu
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Silver, Gary
                                                                                                                                              Yamaka, Miles Yamanaka
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IBM PC compatible
 Sheridan Ross & McIntosh
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73.2%;
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Pred. No. 0.0015;
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COMPUTER: IBM PC OPERATING SYSTEM:
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US-08-485-443B-60
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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LOCATION:
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CITY: D
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STRANDEDNESS: single
                                             COUNTRY:
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                                                                                        1700 LINCOLN ST.,
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                                             USA
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                                                                                                                                         Stiegler, Gary L.
Stiegler, Gary L.
VENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
VENTION: MOLECULES AND USES THEREOF
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                                                                                                           SHERIDAN ROSS
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w, Keith E.
, Shirley Wu
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73.2%;
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Pred. No. 0.0015;
Pred. No. 22;
                                                                                           SUITE 3500
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compatible PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER:

US/08/485,443B

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Best Local Similarity
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                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
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LENGTH: 234 base pairs
TYPE: nucleic acid
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                            ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J.
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: 303 863-9700
TELEFAX: 303 863-0223
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TITLE OF INVENTION: FLEX
TITLE OF INVENTION: MOLE
NUMBER OF SEQUENCES: 190
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                                                                                                                                                                                           COUNTRY: UZIP: 80203
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LOCATION:
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             REGISTRATION NUMBER: :
                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCAGCACGAGGTTTGTTCAAGATCAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                 SSEE: Sheridan Ross & McIntosh
T: 1700 Lincoln Street, Suite 3500
Denyer
                                                                                                                                                                                                                       Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08639075A
                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                    Wu Hunter, Shirley Frank, Glenn R.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Rushlow, Keith E.
DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       Gaines, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                        Stiegler,
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                                                                                                                                                                                                                                                                                                            MOLECULES
                                                                                                                                                                                                                                                                                                           FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                        Gary
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            32,020
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Pred. No. 0.0015;
2618-25-C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6180383
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
                                 INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TOPOLOGY: li
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
                                                                                 TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 80203
                                                                                                                                    NAME: Connell, Gary J. REGISTRATION NUMBER: 3
                                                                                                                                                                                     FILING DATE: <Unknown>
                                                                                                                                                                                                     APPLICATION NUMBER: US 08/639,075
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Colorado
                                                                                                                  REFERENCE/DOCKET NUMBER: 2618-25-C2
                                                                                                                                                    NAME: Connell,
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
LENGTH: 234 base pairs
TYPE: nucleic acid
                                                                 TELEFAX: (303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
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73.2%;
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                                                                    863-0223
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FEATURE:

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TOPOLOGY: linear MOLECULE TYPE: cDNA

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US-09-012-692-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.5
Best Local Similarity 73.2
Matches 60; Conservative
                                                                                                                                                                                               APPLICATION NUMBER: US 08/639
ETILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2610
REFERENCE/DOCKET NUMBER: 2610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                 TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                          CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/639,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 GCGCGTCTCATCTTACAAGATA 129
            NAME/KEY:
                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/012,692 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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LOCATION: 1...
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1700 Lincoln Street, Suite 3500
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                                                                                                                               234 base pairs
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Stiegler, Gary
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Best Local Similarity 73.3
Matches 60; Conservative
108 GCGCGTCTCATCTTACAAGATA 129
                                                       61 AGATGTCTATAAATATAAGAGA 82
                                                                                   1 TCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCAGCACGAGGTTTGTTCAAGATCAA 60
                                                                                                                          5.5%;
                                                                                                            Score 46.8; DB 4;
Pred. No. 0.0015;
0; Mismatches 22;
                                                                                                                                       Length 234;
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Search completed: May Job time : 65 secs 1, 2003, 21:56:13 0;

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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//cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                            0 US-09-291-809C-1
0 US-09-291-809C-3
0 US-09-845-849-3
0 US-09-845-849-3
1 US-09-938-842A-2635
1 US-09-938-842A-1501
0 US-09-938-842A-1538
0 US-10-092-154-380
0 US-09-764-847-380
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1 US-09-764-863-303
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1 US-09-764-863-303
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1 US-09-764-891-243
1 US-09-764-891-2323
1 US-09-925-299-270
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Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 2635, Ap
Sequence 1501, Ap
Sequence 380, App
Sequence 380, App
Sequence 248, App
Sequence 248, App
Sequence 303, App
Sequence 404, App
Sequence 404, App
Sequence 270, App
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CORRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: PCT/US99/08151
PRIOR ETLING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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; NAME/KEY: CDS
; LOCATION: (63)...(588)
US-09-291-809C-1
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     Matches 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Detlef Weigel
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT)
TITLE OF INVENTION: WODIFIED PLANTS HAVING
FILE REFERENCE: SALKINS.026CP1
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Pred. No. 9e-206;
Mismatches 0;
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MODULATED FLOWER DEVELOPMENT
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Sequence 309, App
Sequence 305, App
Sequence 352, App
Sequence 352, App
Sequence 378, Appli
Sequence 403, Appli
Sequence 403, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 184, Appl
Sequence 352, Appl
Sequence 374, Appl
Sequence 352, Appl
Sequence 352, Appl
Sequence 613, Appl
Sequence 6143, Appl
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Database

Minimum DB Maximum DB

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Scoring table: Sequence: Perfect score:

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Sequence 3, Application US/09291809C
Patent NO. US20010049831A1
GENERAL INFORMATION:
APPLICANT: Detlef Weigel
APPLICANT: Salk Institute
TITLE OF INVENTION: MODIFIED PLANTS HAVING M
TITLE OF INVENTION: MODIFIED PLANTS HAVING M
FILE REFERENCE: SALKINS.026CP1
CURRENT APPLICATION NUMBER: US/09/291,809C
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: PCT/US99/08151
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENCTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-291-809C-3
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RESULT 3
US-09-845-849-1
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; Sequence 1, Application US/09845849
; Patent No. US20020029395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR I
; APPLICANT: WEIGEL, Detlef
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Pred. No. 9e-206;
Mismatches 0
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
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TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWI
FILE REFERENCE: SALKINS.026DV1
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TYPE: DNA
ORGANISM: Arabidopsis
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                                      TATAAGTGTGTAATAAAAATGAGAGGGGGAGGAAAATGAGAGTGTTTTTACTTATATAGTG 780
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                                                                                                                                            CCTTTATAACCAATTGATATTGCATACTCTGATGAGATTTATGCATCTATAGTATTTTAA
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CCTTTATAACCAATTGATATTGCATACTCTGATGAGATTTATGCATCTATAGTATTTTAA
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                        TATAAGTGTGTAATAAAAATGAGAGGGGGAGGAAAATGAGAGTGTTTTACTTATATAGTG
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Matches
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
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                                      TCGTGTTTATATTGTTTCGACAGCTTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCC 480
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2635
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Sequence 2635, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
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Best Local Simi
Matches 434;
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2635
LENGTH: 528
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
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Pred. No. 2.1e-85;
0: Mismatches 94;
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GGCTTGGATCTAAGGCCTTCTCAGGTTCAAAACAAGCCAAGAGTTGAGATTGGTGGAGAA

CCTCACCTCCGAGAATATCTCCATTGGTTGGTGACTGATATCCCTGCTACAACTGGAACA 359

CCCTTTCTAAAAGAACACCTGCACTGGATCGTTACAAACATTCCCGGCACAACAGATGCT

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; ORGANISM: Arabidopsis thaliana US-09-938-842A-1501
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CCURRENT APPLICATION NUMBER: US-60/227,866
PRIOR APPLICATION NUMBER: US-60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US-60/264,647
PRIOR FILING DATE: 2001-01-16
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US-09-938-842A-1501
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SEQ ID NO 1501
LENGTH: 534
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APPLICANT:
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APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                              TYPE: DNA
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                                            60 AAGATGTCTATAAATATAAGAGACCCTCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTT 119
                                                                                                                         Local Similarity
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  AATATGGGAACTAGAGTGATAGAGCCATTGATAATGGGGAGAGTGGTAGGAAGATGTTCTT
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                                                                                                Conservative
                                                                                                                       20.7%;
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                                                                                             <u>.</u>
                                                                                                                       Score 176.8; DB 9
Pred. No. 7.8e-35;
                                                                                                Mismatches 197;
                                                                                                                                              DB 9;
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                                                                                                Indels
                                                                                                                                            Length 534;
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US-09-878-574-6398
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098321H1
US-09-878-574-6398
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SEQ ID NO 380
LENGTH: 503
TYPE: DNA
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                           NUMBER OF SEQ ID NOS: 2003
Prior Application removed
SOFTWARE: PatentIn Ver. 2.
                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC009C1
                                                                                                                     CURRENT FILING DATE:
                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/092,154
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Pred. No. 3.7e-09
0; Mismatches 8
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                                                            ; OTHER INFORMATION: n equals a,t,g, or US-09-764-847-380
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APPLICANT: Rosen et al.
   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 380
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Best Local
                              Query Match
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                                                                                      NAME/KEY: SITE
LOCATION: (502)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (503)
                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (502)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION:
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LOCATION: (54)
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                             ENGTH: 503
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les 57; Conserv
               Local
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             Score 49.2; DB Pred. No. 0.01;
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/234,274
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/
FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-0 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/:
FILING DATE: 2000-08-22
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APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/225,447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-01-31
APPLICATION NUMBER: 60/180,628
                                                                                                                                                                                                                  APPLICATION NUMBER: 60/: FILING DATE: 2000-08-30
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APPLICATION NUMBER: 60/244,617
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APPLICATION NUMBER: 60/236,370
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APPLICATION NUMBER: 60/237,039
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APPLICATION NUMBER: 60/229,345
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APPLICATION NUMBER: 60/249,218 FILING DATE: 2000-11-17

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APPLICATION NUMBER: 60/231,243
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Best Local Similarity
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LENGTH: 551
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SEQ ID NO 248
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo :
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
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                                                                                                                                                                                                          LENGTH: 55
                                                                                     NAME/KEY: misc feature LOCATION: (15)
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 Score 48; DB 10;
Pred. No. 0.022;
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                 Length 551;
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; ORGANISM: Homo sapiens
US-09-764-868-303
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US-09-764-868-303
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO5
       Matches
                                        Query Match
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 400
LENGTH: 560
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400, Application US/09925297 Patent No. US20020081659A1
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SEQ ID NO 303
LENGTH: 2585
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                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 928
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                                                                                  OTHER INFORMATION: n equals a,t,g,
                                                                                                         NAME/KEY: misc feature LOCATION: (14)
                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (7)
COTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                       OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                        NAME/KEY: misc feature LOCATION: (10)
   Local Similarity 75.
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Best Local
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SEQ ID NO 404
LENGTH: 631
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 404, Application No.
                                                                                                      Matches
                                                                                                                                                                                           LOCATION: (27)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (28)
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (19)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
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61 AG 62
                                    66 TCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAGGAGTGATGCAGTTATA 125
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                                                                                                    l Similarity
53; Conserv
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10. US20030077808A1
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Perfect score:
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Maximum DB seq length: 2000000000
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SUMMARIES

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Db	Qy	Db	Qy	Db	Qy	D	Оу	Db	Оу	Db.	Qy	Db	ν 0	Db	Qy	B	Qy	В	Qy	Db	Qy	Db	: 5) M	Ве	•	BASE	FEAT	JC	TI	REFE	KEYW	ACCE	госп

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137	GAGTGATT	GTAACCTTTA	GGCCATAA	ACCTCTCTT	CATTAGTC	GGCCTTAGATCCAAGCCATTAGTCACCTCTCTTTGGCCATAAGTAACCTTTAGAGTGATT	GCCTT	196	B 25
197	CCTGAGAA	TTGTTTTGAA	CTCTTGGC	CCAATCTCA	CTTCTCCA	TTCCTGAGGT	TAGAAG	, G	B
660	CCTGAGAA	TTGTTTTGAA	CTCTTGGC	CCAATCTCA	CTTCTCCA	TAGAAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTTGGCTTGTTTTGAACCTGAGAA	TAGAAG	601	Qγ
257	CCAAAGTA	TCCACCATAA	CATCTGGA	GGACTTGGA	GGTTGCTA		TATTCT	⊢	망 :
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317	AATGGAGA AATGGAGA	AGTCACCAACC AGTCACCAACC	GGATATCA	GTTGTAGCA GTTGTAGCA		ATCTCATTGCCAAAGGTTGTTCCAGTTGTAGCAGGATATC 	ATCTCA	481 376	B 12
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480	3=8	AGTGGGACTTGGATTTTCGTAACAC	TGGGACTT	ACACGATGAATTCCTGCA	CACGATGA	AAACACG	AACAATAT	. 421	P 09
437	GCTGTCGA	ACCCTGGTGCATACACTGTTTGCCTGCCAAGC	PACACTGTT	CCTGGTGCA	α-	GTTGAAGTTCTGGCGC	CGAGTG	496	Dβ
420	GCTGTCGA	TGCCTGCCAA	PACACTGTT	CCTGGTGCA	GCGCCAC	- വ്	CGAGTG	361	οy
497	CAAACTCG		CGAGATTG	ACGGGAAGG	CIGCGGCC	AATTGTAGAAAA	TGACAAT	556	Дb
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557	CTCTCCCTC	AGCCAC	CTTCTTCCT	AAGAAGCCATCTAAAGTCTTCTTCCTCCGC	AAGAAGCC	GTTATAAAGG	C-ATTG	615	В
300	rerecere	AGCCAC	CTTCTTCCT	ATCTAAAGT	AAGAAGCC	ATAAAGG	TIG	241	Qy
616	ATGCAATAT ATGCAATAT	ATCAGAGT	CATAAATCTC	ACTATAGATGO 	ATTAAAATA ATTAAAATA	GTTATTAA GTTATTAA	TAAAATG TAAAATG	675	D 64
7	TCGTATCA	STTCGTTAC	ი-	TACTATAGGC	ATATTGAACTA	TACACACTTATA	TA-	735	DЬ
180	TCGTATCA	STTCGTTAC	CATCATCAC	TACTATAGG	TATTGAAC	ACTTAT	TTATTACAC	121	Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Araki,T. and Kobayashi,Y.

Direct Submission

Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:trarqui@gr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136, Fax:81-75-753-4141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi,Y., Kaya,H., Goto,K., Iwab
A pair of related genes with antagon
flowering signals
Science 286 (5446), 1960-1962 (1999)
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                                                                                                                     /protein_id="BAA77838.1"
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/db_xref="GI:4903012"
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/translation="MSINIRDPLIVSRVVGDVPSPSNPHLREYLHWLVTDLPATTGTTFG
PSQVQNKPRVEIGGEDLRNFYTLVMVDDDVPSPSNPHLREYLHWLVTDLPATTGTTFG
NEIVCYENPSFTAGIHRVVFILFRQLGRQTVYAPGWRQNFNTREFAEIYNLGLPVAAV
                                                                                                                                                                                                                  similar to mammalian phophatidylethanolamine protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"
                                                                                                                                                                                                                                                                                                                                                          /note="Corresponds to nucleotides 10511-10780,
11596-11657, 12371-12411, and 12536-13005 of F5114
(Accession Number AC001229)"
                                                                                                                                                                                                                                                                       /gene="FT"
/standard_name="FLOWERING LOCUS T"
/note="induces flowering; loss-of-function mutation
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/db_xref="taxon:3702"
/chromosome="1"
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Arabidopsis thaliana p FT (At1g65480) mRNA, c AY065378 AY065378.1 GI:1752918

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mediating

PLN 26-APR-2002 protein

GI:17529185

AY065378

FLI_CDNA.

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                                    TTAAACGGATCAAGAACGTCTCCAACAACTCTGCTTACTATAAGAGGGGTCTCTTATATTT
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RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI CDNAs (RAFI CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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PSOVQNEPRVEIGGEDLRNFYTLVMVDPDVPSPSNPHLREYLHWLVTDIPATTGTTFG
NEIVCYENPSPTAGIHRVVFILFRQLGRQTVVAPGWRQNFNTREFAEIYNLGLPVAAV
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(Lambda ZAP) as a XhoI/SstI insert.
ecotype: Columbia"
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/product="putative flowering signals mediating
/protein_id="AALJ8819.1"
/db_xref="GI:17529186"
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/db_xref="taxon:3702"
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2 (bases 1 to 780)
Araki, T. and Kobaya
Direct Submission
                                            A pair of related genes with antagon
flowering signals
Science 286 (5446), 1960-1962 (1999)
                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:taraqui@gr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136, Fax:81-75-753-4141)
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/db_xref="GI:4903014"
/db_xref="GI:4903014"
/translation="MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLR
/translation="MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLR
/translation="MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLR
/translation="MSINIRDPLIVSRVC"
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/note="amino acid residues 1-101 of hypothetical
translation product are identical to those of FT protein
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11596-11657, 12371-12411, and 12536-13005 of F5T14
(Accession Number AC001229)"
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/db_xref="taxon:3702"
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2 (bases 1 to 559)
2 ramada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.N. Yamada, K., Chan, M.M., Chang, C.C., Toriumi, M., Wallender, E.K., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H. Cheuk, R., Hayashizaki, Y., Jishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kahida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kahida, J., Jan, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M. Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M. Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 559)
1 (bases 1 to 559)
2 manda, K., Chan, M.M., Chang, C.H., Dale, J.M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida, Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY133813

Arabidopsis thaliana clone U11796 putative flower mediating protein FT (Atlg65480) mRNA, complete
                                                                                                                                                    Direct Submission Submitted (17-JUL-2002) Plant Gene Expression Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                 Ishida, J.,
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The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAS: Yamada, K., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M. Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Kariin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and

Yamada,K.

(SSP/PGEC)

and

Seki,

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(RIKEN GSC)

contributed equally

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                    CTCTTATATTTATAGACAT
                                                                                               GAGAAGGCCTTAGATCCAAGCCATTAGTCACCTCTCTTTTGGCCATAAGTAACCTTTAGAG
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                                                           TGATTGATCTATTAAACGGATCAAGAACGTCTCCAACAACTCTGCTTACTATAAGAGGGT 775
                                                                                       GAGAAGGCCTTAGATCCAAGCCATTAGTCACCTCTTTGGCCATAAGTAACCTTTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative flowering signals mediating protein FT"
/protein_id="AAM91747.1"
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NEIVCYENPSFTAGIHRVVFILFRQLGRQTVYAPGWRQNFNTREFAEIYNLGLPVAAV
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117 c 132
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/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At1g65480"
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CTCTCTTTGGCCATAAGTAACCTTTAGAGTGATTGATCTATTAAACGGATCAAGAACGTC
         CTCTCTTTGGCCATAAGTAACCTTTAGAGTGATTGATCTATTAAACGGATCAAGAACGTC
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Query Match
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Matches 528; Conserv
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RS Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.

Method for shortening plant generation and plant

Patent: JP 2000139250-A 1 23-MAY-2000;

TORAY IND INC

S Arabidopsis
PN JP 2000139250-A/1
PD 23-MAY-2000
PF 11-NOV-1998 JP 1998320219
PF 11-NOV-1998 JP 1998320219
PR

PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
A0111/00, A01H5/00, C12N5/10, C12N15/09//(C12N5/00, C12R1:91), PC
(C12N15/09, C12R1:91)
CCC (C12N15/09, C12R1:91)
CCC (C12N15/00, C12R1:91)
FH Key

I Location/Qualifiers
FT Source
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GGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGCGCCACCC 386
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Arabidopsis
Arabidopsis
Arabidopsis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae.
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/db_xref="taxon:3701"
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gene

	CDS	gene		CDS	gene		FEATURES source	Direct L Submitt On Jun	Street, Alba REFERENCE 5 (bases 1 AUTHORS Theologis, A.	-	RS	_	SE	TITLE Direct JOURNAL Submitt			AUTHORS VYSOTSK Shen,Y.I Kim,C.		SOURCE Arabidopsis ORGANISM Arabidopsis Eukaryota;	ACCESSION AC001229 VERSION AC001229.1 KEYWORDS HTG.	F5I14/c LOCUS F5I14 DEFINITION Sequence complete	RESULT 8	Qy 747 TCCAACACC Db 48 TCCAACAACC
/gene="p5114.2" /gene="p5114.2" /Codon_start=1 /evidence=not_experimental /protein_id="AAB60903.1" /db_xref="G1:2190539" /translation="MDEVSTVEENEN SSINLEMKGLFDYFREVMDKSKRTDL	/yene- £3114.2 complement(join(1312170	/translation="MRRQPKSELFPK. QCKPSSSNRKKSRRVKQLLQFDKSCR LVKAFQIVRKMKTKVWKKDVQRLMMK complement(13122949)	<pre>/codon_start=1 /evidence=not_experimental /protein_id="AAB60919.1" /db_xref="GI:2190555"</pre>	complement(join(129327,950./gene="F5I14.1"	/cmplement(1291191)	lumbia" on:3702"		ssion 1-JUN-1997) 1997 this sequence	Albany, CA 94710, USA es 1 to 109560) is,A.	Direct Submission Submitted (06-JUN-1997) Plant Gene	es 1 to 109560) is,A.	-1997) Plant Gene A 94710, USA	Street, Albany, CA 94710, USA 3 (bases 1 to 109560) Theologis, A.	Gene	sned (1997) es 1 to 109560)	Lel, N.A. and Theologis, A. Lence of BAC F5I14 from Arab	Vysotskaia, V.S., Osborne, B.I., Toriumi, M., Yu, G., Oji, Osborne, B.I., Toriumi, M., Yu, G., Oji, Osborne, Y.K., Buehler, E., Conway, A.B., Conway, A.R., Dewar Kim, C., Kurtz, D., Li, Y., Shinn, P., Sun, H., Davis, R.W.,	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops 1 (bases 1 to 109560)	osis thaliana. osis thaliana ta; Viridiplantae; Streptoph	9.1 GI:2182285	109560 bp DNA e of BAC F5I14 from Arabidopsis e sequence.		TCCAACAACTCTGCTTACTATAAGAGGGTCTCTTATATTTATAGACAT
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VDEI -		FDGR YRKK								nan		nan		nan		1	R.,		ta;		1997		

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DKMKEEEALKRRLNARMEYAKFLQDTVKEMAKEVQTSRSGETKKTAEDLDGFMTKVRR

gene

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complement(40241. .40963)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(41498. .41562,41619. .41734,41808. .41896
41981. .42127,42220. .42267,42316. .42564,42795. .42875))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSQKDVALDEMMASTAKDANEQAKAKTLEKHEQLCELSRALAVLASASVWRLLTTLSF
ILPIGVLRSVSMEREEFLKLVKKEVDLYNSMVEKGGTDDEEDARKAYLAAREDSDRSA
QKAIADKTSSALLDRVETMLQKLEKEIDDVDNKIGNRWRLLDRSVDYDGKVSPDEVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(40241. .40963)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIVCYENPSPTAGIHRVVFILFRQLGRQTVYAPGWRQNFNTREFAEIYNLGLPVAAV
FYNCQRESGCGGRRL"
                                                                                                                                                                                                                                                                  /note="Similar to Saccharomyces hypothetical protein
p9642.2 (gb|U40828)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VD I RSFMDNMMQKNSSEMAEKDSKREEKLLLKQLEKNRCEAEKEKKRMERQVLKEKLQ
QEKEQKLLQKA I VDENNKEKEETESRKR I KKQQDESEKEQKRREKEQAELKKQLQVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLKLKEKTESVTMVAVKSAVVSVGQRVSYGVLNVDADVLEDDSESCLWCWETRDLKIM
PSSVRGVLKLRRTCRKKIHERITAVSAMLAALQREETEKLWRSDLSKAAEKLGKILSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAMYLKDTLGKEGIQELIQNLSKDKVFVVFRWQNTGGRLSEVSERD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F5I14.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to Arabidopsis TFL1 (gb|U77674)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(10580. .10780,11596. .11657,12371. .12411,12536. .12759)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F5I14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="EST gb|N37484 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .37445
                                                                                                                                                                                                                                                                                                                                                                                                                                                            75. .44922)
                                                                                                                                                                                                                                                                                                                                                                  5. .43043,43213. .43339,43501. .43593, .44002,44168. .44480,44564. .44922))
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12940
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                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                  AGTAAAACACTCTCATTTTCCTCCCCCTCTCATTTTTATTACACACTTATATATTGAACT 145
                                                                                                                    TATAAATATAACACTTCATTTCATGTAGATTAATAATTATCGCATCACACACTATATA 12941
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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CFLVKNLYLSCDPYMRGRMRDFHGSYLPPFVPGQKCCEVLREVLFIGELFIFEEREMC
RCCIYALERSCTPSFRCFDEMIYYMLRKIGITYILVKLFIFENDSLISTDSFVILMQ
RCCIYALERSCTPSFRCFDEMIYYMLRKIGITYILVKLFIFENDSLISTDSFVILMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIEGFGLARVIDSDDTNYKPGDIVSGIIGWEEYSLLRSSDNLQLRNIQLDDDIPLSYH

IGLLCWAGFTAYAGFNEICCFKKGDSVEVSAACGAVGQLVGQLAKLHCCYVVGSAGSK

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GRIALCGMVSLQSLSTSSQGIKNLYSALYKRLBLEGFLQSDYLHIFPQFLENVKRYYK

EGKIYYVEDISEGLDLAPAALVGLFSGKNIGKQVVRVAKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(50678. .51059,51406. .51488,51567. .51733,
51818. .52033,52078. .52294,52510. .52743))
/gene="F5114.9"
/note="Strong similarity to Arabidopsis
zeta-crystallin-like protein (gb|249268)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTKIGSRRVIQISAAFMIFFSIFGKFGAFFASIPLPIMASLYCIVLCFVCKSFSSHHI
CSIAFSINICFIFFTKIKSNSIYNAASVGLSYLQFCNLNSFNIKFILGFSFFMAISIP
QYFREYYNGGWRSDHHSNWVSISYSIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCFOVLICILGVWRNIVRFLSPLSIAPLATFTGLGLYHIGFPLIYNMMQTSFIFOLAR
CVEVGLPGLILLIENTQYLPRFLKMKKOVMILDGSFCORYGMICIFLYWLFAQLLTS
SGVYDHKSHTTQTSCRFDTGLITNFFWIYILYFYPFQWSCPFFDITDSFRAMAASFFTL
FESTGLFYASARYGSATPIPPSVVSRGTCWLGVGVLLNGMLGGITGITTSTENVGLLA
                                                                                                                                                                                                                                                                                                                                                                                       NVKIKGVLSLNSQLFHIAINRCRNIKIEDVRIIAPDESPNTDGIHIQLSTDIEVRNAS
IKTGDDCISIGPGTKNLMVDGITCGPGHGISIGSLAKSIEEQGVENVTVKNAVFVRTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (50678. .52743)
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VLGFQHYLLSLGITVLIPSMLETFFFFFFFFLNRESILIFYAEKVKVIQTLLFVSGLT
TLFQSFFGTRLPVIAVASYAYIIPITSIIYSTRFTYYTDPFERFVRTMRSIQGALIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(47061 ...47422,47541 ...47632,47766 ...47824,47929 ...48015,48122 ...48218,48320 ...48525,48704 ...48799,48184 ...489595,49953 ...49153,49242 ...49418,49467 ...49532,49587 ...49587 ...49587 ...49587 ...49587
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IKKDDKLIKAEGVESLSEAELRQACRERGMLQLGSVEEMREQLVDWLDLSLNHSVPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                         IYSGIMGTSATEIAIKMDCSEKVPCTGIRMQAINLTSYGEAAKTSCTNVSGKQLGLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
                                                                                                                                                                                                                                                                   54.4%;
                                                                                                                                                                                                                                                                Score 466; DB 8; L; Pred. No. 8.3e-100;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                               Length 109560;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2483)
Kardailsky,I. and Weigel,D.
Direct Submission
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Kardailsky,I., Shukla,V.K., Ahn,J.H., Dagenais,N.,
Christensen,S.K., Nguyen,J.T., Chory,J., Harrison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana. Arabidopsis thaliana
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/note="similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PEBP) and Raf kinase inhibitor protein; corresponds to Arabidopsis thaliana BAC F5I14 sequence
                                                  /function="induces flowering"
/note="similar to hippocampal
                                                                                                                                                                                         join(1. .2
/gene="FT"
                                                                                   /gene="FT"
                                                                                                                                 /gene="FT"
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/chromosome="I"
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                                                                                                                                                                  Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Araki,T. and Koba
Direct Submission
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TSF.
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Science 286
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                                                                                                                           Kobayashi,Y., Kaya,H.,
                                                                                                                                                                                                                                                                     AB027506
                                                                                                                                                          Rosidae;
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                                                                                            pair of related genes with antagonistic lowering signals
                                                (bases 1 to 799)
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                              and Kobayashi,Y.
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PSQVQNKPRVEIGGEDLRNEYTLVMVDPDVPSPSNPHLREYLHWLVTDIPATTGTTFG
NEIVCYENPSPTAGIHRVVFILFRQLGRQTVYAPGWRQNFNTREFAEIINLGLPVAAV
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/protein_id="AAF03936.1"
/db_xref="GI:6117978"
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(19-MAY-1999) Takashi Araki,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 CATCACCGTTCGTTACTCGTATCATAAAATGGTTATTAAAATTAAAATA---CTATAGATG 213
                                                                        TGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGAGGTCTTCTCCACCAAT
                                                                                                                                  AGCAGGGATATCAGTCACCAACCAATGGAGATATTCTCGGAGGTGAGGGTTGCTAGGACT. 569
                                                                                                                                                                                           TGCAGTGGGACTTGGATTTTCGTAACACACAATCTCATTGCCAAAAGGTTGTTCCAGTTGT
                                                                                                                                                                                                                                                                TGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGACACGATGAATTCC
                                                                                                                                                                                                                                                                                                              AAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGCGCCACCCTGG
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CTCCACTATTGGTTTGTTCAGAACTTGAGAAGGCCTTAGATCCAAGCCATTAGTAACCTC
                           CTCAACTCTTGGCTTGTTTTGAACCTGAGAAGGCCTTAGATCCAAGCCATTAGTCACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kyoto University, Department of Botany, Division of Biological
Sciences; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:taraqui@gr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:81-75-753-4141)
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/gene="TSF"
a 152 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="extensive homology with FT similar to mammalian phophatidylethanolamine protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"
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32. .559
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/chromosome="4"
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/strain="Columbia"
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76.6%;
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                                                     CTAAAGTCTTCTTCCTCCGCAGCCACTCTCCCTCTGACAATTGTAGAAAACTGCGGGCCAC 326
             GGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGCGCCACCC
AGGAAGACCAAGATTGTAGATCTCAGCAAACTCACGAGTGTTGAACTGTTGGCGCCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-MAY-1999) Plant Biology Laboratory, Institute for Biological Studies, 10010 N. Torrey Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activation tagging of the floral inducer Science 286 (5446), 1962-1965 (1999)
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Christensen,S.K., Nguyen,J.T., Chory,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Haaksma,S., Shukla,V.K.,
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nilarity 82.2%;
Conservative
                                                                                                                                                                                                                                                                                                                /note-"flowering locus T (FT) homolog; similar to hippocampal cholinergic neurostimulating peptide (HC precursor, phosphatidylethanolamine binding protein and Raf kinase inhibitor protein"
                                                                                                                                                                                     NEVVCYESPRPPSGIHRIVLVLFRQLGRQTVYAPGWRQQFNTREFAEIYNLGLPVAAS
YFNCQRENGCGGRRT"
. 116 c 142 g 147 t
                                                                                                                                                                                                                             /translation="MSLSRRDPLVVGSVVGDVLDPFTRLVSLKVTYGHREVTNGLDLR
PSQVLNKPIVEIGGDDFRNFYTLVMVDPDVPSPSNPHQREYLHWLVTDIPATTGNAFG
                                                                                                                                                                                                                                                           /product="twin sister of
/protein_id="AAF03937.1"
/db_xref="GI:6117980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis/cultivar="Columbia"
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/chromosome="IV"
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TORAY IND INC
OS Arabidopsis
PN JP 2000139250-A/2
PD 23-MAY-2000
PF 11-NOV-1998 JP 1998320219
PR TAKASHI ARAKI KYOJI KOBAYASHI KENICHI OG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAACAACTCTGCTTACTATAAGAGGGTCTCTTATATTTATAGACAT 794
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/db_xref="taxon:3701"
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                                                                                                                                                                              Submitted (17-MAY-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu; Okitsu, Shimizu, Shizuoka 424-0292, Japan (E-mail:om9330@okt.affrc.go.jp, Tel:81-543-69-7108, Fax:81-543-69-2115)
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                          Citrus unshiu (strain:Miyagawa-wase satsuma mandarin) stage juice sac and pulp segment cDNA to mRNA. Citrus unshiu
                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                     2 (bases 1 to 745)
Omura, M., Kobayashi, Y. and Araki, T.
                                                                                                                                                                                                                                                                                Science 286 (5446), 1960-1962 (1999) 20050958
                                                                                                                                                                                                                                                                                                          Kobayashi,Y., Kaya,H., Goto,K., Iwabuchi,
A pair of related genes with antagonistic
flowering signals
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                             /gene="CifT"
96. .629
                                                                                                            /organism="Citrus unshiu"
/strain="Miyagawa-wase satsuma
/db_xref="taxon:55188"
                                                                    /dev_stage="developing stage juice sac and pulp segment"
/note="partial sequence (pcMFRI727.131) is deposited in
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  Floral development genes
Patent: WO 0244390-A 11 06-JUN-2002;
E. I. du Pont de Nemours and Company
                                                                             Cahoon, E.B., Cahoon, R.E.,
                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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PSEVLNQPRAEEIGGDDKFTYYTLVMVDPDAPSPSDPSLREYLHWLVTDIPATTGASFG
OEIVNYESPRPTMGIHRFVFVLFRQLGRQTVYAPGWRQNFSTRDFAELINLGPPVAAV
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Pred. No. 5.1e-58;
0; Mismatches 144;
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                                                                                                                             mRNA.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                   AB052943
AB052943.1
2 (bases 1 to 847)
Yano,M. and Kojima,S.
Direct Submission
Submitted (33-DEC-2000) Masahiro Yano, National Institute of Agrobiological Resources, Department of Molecular Genetics; Kannondai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                              AB052943 847 bp ml
Oryza sativa (indica cultivar-group)
cultivar:Kasalath.
                                                                                    Unpublished
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                                                                                                             Kojima, S., Monna, L., Fuse, T., Sasaki, T. and Yano, M. Hd3a, a quantitative trait locus, involves in the p
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Fax:81-298-38-7468)
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/protein_id="Bab61029.1"
/db_xref="GI:14517622"
/translation="MAGSGRDRDPLVVGRVVGDVLDAFVRSTNLKVTYGSKTVSNGCE/translation="MAGSGRDRDPLVVGRVVGDVLDAFVRSTNLKVTYGSKTVSNGCELKPSMVTHQPRVEVGROHNRTFYTLVMVDPDAPSPSDPNLREYLHWLVTDIPGTTAAS
EGQEVMCYESPRPTMG.HRLVFVLFQQLGRQTVYAPGWRQNFNTKDFAELYNLGSPVARVYFNCQREAGSGGRRVYN"
228 c 224 g 194 t
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/cultivar="Kasalath"
/db_xref="taxon:39946"
/chromosome="6"
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Pred. No. 2.8e-48;
0; Mismatches 166;
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Maximum DB seq length: 2000000000
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692.4
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Match
      100.0
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2. \SIDS2/gcgdata/geneseq/geneseqn-embl/WA1981.DAT: *
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                                                                                                                                                         Length
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                   AAZ28490
AAZ28491
AAC34682
AAC48359
AAA60683
AAC42966
AAA60684
AAC90636
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Flowering locus T
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Strawberry floweri
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5.6	•	•	•	5.6	5. 6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5. 8	5.9	5.9	6.0	6.0	6.1	6.2	6.5	7.4	8.4	9.3	9.6	13.6	7.	8	20.4	0		20.6	20.6
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ABN73981	ABN73980	AAH34361	AAF16381	ABN74051	AAS28106	ABK28390	AAK62481	ABQ54500	AAD34120	ABN74279	ABA77106	ABQ67094	ABA77091	ABN74030	ABK41982	AAK60828	ABL34609	AAH35052	ABN74181	ABN73995	AAZ30973	AAD17465	ABQ55599	AAC90667	AAQ14832	AAT60142	AAC90666	AAT60139	AAV66749	AAC90668	ABK82094	ABK82122	ABK82092	ABK82091	ABK82093
Bovine embryonic g	m .	Human colon cancer	Human prostate can	Bovine embryonic g	Novel cDNA encodin	DNA transcription	Human immune/haema	Human ovarian anti	Human secreted pro	Bovine embryonic g	Proliferative glom	Human angiogenesis		Bovine embryonic g	cDNA encoding nove	Human immune/haema	Human metastasis a	colon cance			Porcine complement	Spinach lycopene e	Human ovarian anti		OV-16 antigen. On		Strawberry floweri			\mathbf{L}				ncoding	Novel floral meris

ALIGNMENTS

ВP

RESULT 1
AAZ28490/c
ID AAZ284
XX AAZ284
AC AAZ Weigel D; (SALK) SALK INST BIOLOGICAL STUDIES 15-APR-1998; 13-APR-1999; 21-OCT-1999 WO9953070-A1. Arabidopsis thaliana. Flowering locus T gene; FT; flowering time; modulator; early flowering; antibody; cellular binding protein; crop; ss. Flowering locus T (FT) gene 98US-0060726 99WO-US08151 /product= FT /note= "Flowering locus T" Location/Qualifiers 63..590 /*tag= a

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                              CAATTGGTTATAAAGGAAGAAGCCATCTAAAGTCTTCTTCCTCCGCAGCCACTCTCCCCTC
GGCCTTAGATCCAAGCCATTAGTCACCTCTCTTTGGCCATAAGTAACCTTTAGAGTGATT
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DB; AAY49098.
                    TAGAAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTTGGCTTGTTTTGAACCTGAGAA
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Pred. No. 3.8e-190;
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Query Match Best Local Matches

Similarity

100.0%; A

; Score 856; E; Pred. No. 3.8

BB T;

Length Indels

,8e-190; 20; 0 other;

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194 C;

150 <u>ი</u> 263

Conservative

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CTCGAGTTTTTTTTTTTTTTTTTTATAAATATAACACTTCATTTCATGTAGATTAATA

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                      rhis is the flowering locus T (FT) gene antisense polynucleotide sequence. This sequence is used in the production of the antisense construct of the invention pSKIO60. FT regulates flowering in plants by modulating flowering time. Overexpression of FT results in early flowering, while loss of function mutations or antisense directed to FT causes late flowering. The FT polypeptide has a molecular weight of approximately 20kD, and is located on chromosome 1. The FT polypeptide is used in the invention to modulate flowering time in many mono and di-cotyledonous plants. The FT polypeptide sequence is used for recombinant production of the polypeptide, and as a source of antisense, ribozyme or triplex forming sequences. The FT polypeptide can also be used to raise antibodies and to screen for modulators or cellular binding proteins. The methods of the invention allow for the production of crops at any time of year.
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antibody;
                                                                                                                                                                                                                                                        New flowering locus T polypeptide that regulates flowering particularly used to accelerate flowering
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RESULT 3
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ID AAC34682 standard; E
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AC AAC34682;
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DT 17-OCT-2000 (first
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DE Arabidopsis thaliana
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DE Hybridisation assay;
KW protein identificati
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           Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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DB; AAB12459.
                                                                                                                                                             CTCTCTTTGGCCATAAGTAACCTTTAGAGTGATTGATCTATTAAACGGATCAAGAACGTC
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                                                  TCCAACAACTCTGCTTACTATAAGAGGGTCTCTTATATTTATAGACAT
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Pred. No. 1.1e-113;
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Pred. No. 1.2e-78;
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Best Local S
Matches 432
                                                                                                                                                                                                           the present invention describes a method to accelerate plant generation and generation accelerated plants. The method uses a controlling gene functioning in the downstream of a gene under the control of solar radiation to accelerate plant generation using a gene functioning to accelerate the flowering time regardless of solar radiation. The method can control flowering time to a desired period by shortening the juvenile stage. The present sequence represents a specifically claimed Arabidopsis nucleotide sequence, which is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method to accelerate plants -
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                                                                                                                                             Sequence
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                                      al Similarity
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                                Novel nucleic acid involved in controlling plant flowering processes useful for generating transgenic plants, in particular strawberry plants having altered flowering behavior such as early, delayed or day-neutral flowering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the nucleic acid and protein sequences of a number of proteins from the strawberry which are involved in the regulation of flowering. These were identified using primers based on the homologous sequences from A. thaliana, B. napus and R. sativus. They can be used in the production of transgenic field crops whose flowering is regulated and the time of fruiting and harvesting can be manipulated.
                                                                                          Terminal flower 1; tfl1; transgenic plant; ss.
                                                                        Arabidopsis
                                                                                                                        Arabidopsis
                                                                                                                                             24-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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A cDNA clone (AAT60140) codes for the terminal flower1 (TFL1) protein (AAW13945) of Arabidopsis thaliana. It was obtd. from an Arabidopsis expressed sequence tag, clone 129D7T. A genomic till clone (AAT60142) has also been obtd. The wild-type role of the till gene is to inhibit flowering and to prevent the apical meristem from switching to a floral fate. The till gene was identified as a homologue of the Antirrhinum centraradialis gene (see also AAT60141). The flowering characteristics of transgenic plants, esp. switching of apical meristem to a floral fate and the timing of flowering, can be manipulated by regulating cen or till gene expression.
                                                                                                                                                                                                                                                                              Antirrhinum majus centroradialis gene and Arabidopsis homologue, Tfll - control switching of apical meristem to floral fate, use in plant hybridisation and in control of growing season
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GAACCTGAGAAGGCCTTAGATCCAAGCCATTAGTCACCTCTCTTTGGCCATAAGTAACCT
                            TCACCAAAGTGAAGAAGGATCTGAGATCACCACCATGGATCTCAACCCTAGGCTTGGAGG
                                             TAACCAAAGTATAGAAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTTGGCTTTTT
                                                                                     TCCAGTGCAGGTGTTCTTTTAGAAAGGGGTCACTAGGACCTGGAACATCTGGGTCTATCA
                                                                                                 ACCAATGGAGATATTCTCGGAGGTGAGGGTTGCTAGGACTTTGGAACATCTGGATCCACCA 589
                                                                                                                                             CATAGCTCACCACCTCTTTGCCAAACGTAGCATCTGTTGTGCCGGGAATGTTTGTAACGA
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The invention describes a substantially purified or isolated polypeptide CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and WADS-like proteins, or their functionally active fragments or variants. CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a construct (III) population (II), or a certor (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant. The CC which involves introducing (II), (III) or (IV) into the plant. The CC which involves introducing (II), (III) or (IV) into the plant. The CC individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., CC enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. CC Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass fescue species, useful for controlling plant life cycles and/or growth.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flowering plant architecture has a wide range of applications such a inducing male sterility for hybrid seed production; changing flowering architecture for enhancing value of ornamentals; delaying flowering forage grasses thus stopping the formation of less digestible stems increasing herbage quality; altering flowering time allowing early
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GAGAACTTCTCCAATGACACGACCAACAATAAGAGGCTC
              TTCCAGTTGTAGCAGGGATATCAGTCACCAACCAATGGAGATATTCTCGGAGGTGAGGGT
                                                                                                                                                                                                                                                                                                                      TGTGGATTCCAATGTTGGGCTTTGGGCTCTCATAGCTCATGACCTCCCCCCCAAATGAAG
                                                                                                                                                                                                                                                                                                                                        TAGTCACC---TCTCTTTGGCCATAAGTAACCTTTAGAGTGATTGATCTATTAAACGGAT
                                                                                                                                                          CTCCACCAATCTCAACTCTTGGCTTGTTTTGAACCTGAGAAGGCCTTAGATCCAAGCCAT
                                                                                                                                                                                         CACTTGGTCCTGGCACATCTGGGTCCGCCATAACCAATGTGAATAAGGATCGCAAGTCAC
                                                                                                                                                                                                                       TGCTAGGACTTGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGAGGTCTT
                                                                                                                                                                                                                                                        CATCTGTTGTCCCAGGTATATTACTGACAATCCAGTGAAGATGCTCCCGCAGATACGGAT
                                                                                                                                                                                                                                                                                                                                                                                     TGAAGGAAGGCACAGATACAGTCTGCCTTCGCTTCTGCTTGAAGAGCACAAAAATGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCACAGGGAGGCCAAGATCATTATCCACAGCAAACTGGCGGGTGTTGAAATGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGC
                                                               TGAAGACCAGCTTGTTTGAGTTATAGGTTGCTACCATCTTCACACATGGGTTAAATGGAT
                                                                                                                            CCCCCTGAACCTCTACTCTTGGTTTAGATACAACTGCTGATGGGTAGAGCTCATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCCTGGTGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 176; DB 24;
Pred. No. 1.4e-31;
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103
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                                                                                                                                                                                                                                                                              C(1) from a rygrams (Lolium sp.) or fescue (Festucas sp.) species, such as C(MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, Homeo-box proteins (HB) CC and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (II) comprising (II), or a construct (III) comprising (II), or a cycles architecture and/or flower and/or inflorescence development in a plant, children for architecture and/or flower and/or inflorescence development in a plant, conditionally activities may alter flower, embryo and seed development. The cordination of samultaneous enhancement or downregulation or Ands-box corgan identity through conversion of one floral organ in another. CC manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. CC through conversion of one floral organ in another. Plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower for architecture for enhancing value of ornamentals; delaying flowering in activity altering architecture. Manipulation of corpus; delaying vegetative phase to increase biomass production; changing those architecture for enhancing value of ornamentals; delaying flower in activity altering architecture. Manipulation of corpus; delaying vegetative phase to increase biomass production; changing corpus; delaying vegetative phase to increase biomass production; changing corpus; delaying vegetative phases to increase biomass production; changing carly corpus; delaying vegetative phases to increase biomass production; change and reducing corpus; delaying vegetative phases to increase biomass production; change of allering plant to enhanced business in fruit trees; altering plant carrier for manipulation plant life cycles.
                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGRI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a substantially purified or isolated polypeptide from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as 5-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
                                                                                                                                             AAGCCATCTAAAGTCTTCCTTCCGCAGCAGCTCTCCCCTCTGACAATTGTAGAAAACTG 319
                                                                  CGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGC
                                                                                                                  GCCACCCTGGTGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGACAC
                                        CAGCCACAGGGAGGCCAAGATCATTATCCACAGCAAACTGGCGGGTGTTGAAATGATCCC
                                                                                                                                                                                                                                                                                                                for manipulating plant life
                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                            196 A; 181 C;
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                                                                                                                                                                                                                 Score 176; DB 24
Pred. No. 1.4e-31
                                                                                                                                                                                                                                                                          181 G;
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                                                                                                                                                                                                                                                                                                                                                                               CEN: CEN-like protein; APETALA2; AP2; AP2-like protein; HB; HB; HOmeo-box protein; HB-like protein; plant growth; plant architecture; inflorescence development; flower development; embryo development; seed development flower organ identity; phase change; male sterility; hybrid seed production; herbage quality; early maturing crop; biomass increase; branching increase; blocking flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002
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                                                                                                                                    WPI; 2002-452388/48
                                                                                                                                                             Spangenberg G,
                                                                                                                                                                                                                                19-OCT-2000; 2000AU-0000873
                                                                                                                                                                                                                                                         17-OCT-2001; 2001WO-AU01311
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                                                                                                                                                                                                                                                                                                                                                                    allergenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel floral meristem identity gene LpCENa contig #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                    pollen;
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New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or fescue species, useful for controlling plant life cycles and/or growth

The invention describes a substantially purified or (I) from a ryegrass (Lolium $\operatorname{sp.}$) or fescue (Festuca

isolated polypeptide
sp.) species, such a

such as

Claim 4; Fig 32;

290pp; English

CENTRORADIALIS, fescue species,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sin
Matches 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and construct the proteins (II) is useful for modifying plant life cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 792 BP; 196 A; 181 C; 182 G; 231 T; 2 other;
145
                                                                                                                                                                                                                                                                                                                                                560 TGCTAGGACTTGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGAGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                   385 CATCTGTTGTCCCAGGTATATTACTGACAATCCAGTGAAGATGCTCCCGCAGATACGGAT
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                                               CAAGAACGTCTCCAACAACTCTGCTTACTATAAGAGGGTC 776
                                                                                            TGAAGACCAGCTTGTTTGAGTTATAGGTTGCTACCATCTTCACACATGGGTTAAATGGAT
                                                                                                                                            TAGTCACC - - - TCTCTTTGGCCATAAGTAACCTTTAGAGTGATTGATCTATTAAACGGAT
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Pred. No. 1.4e-31;
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ABK82122/c

ID ABK82122 standard; cDNA; 1225 BP
XX

ABK82122;

XX

DT 27-AUG-2002 (first entry)

XX

DNA encoding novel floral merist
XX

Ryegrass; fescue; MADS-box; MADS
KW CEN; CEN-like protein; HB-like prote
KW inflorescence development; flower
KW CEN; CEN-like production; herbage
KW biomass increase; branching incr
KW MO200233091-Al.

PN WO200233091-Al.

PN WO200233091-Al.

PN WO200233091-Al.

AX

In-cct-2001; 2000AU-0000873

XX

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In-cct-2001; 2000AU-0000873

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PR 19-OCT-2000; 2000AU-0000873

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AA (AGRE-) AGRESEARCH LTD.

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PR 19-OCT-2001; 2001WO-AU01311.

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PR 19-OCT-2001; 2000AU-0000873

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CO The invention describes a substic contribution of contri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGRIC VICTORIA SERVICES PTY LTD AGRESEARCH LTD.
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New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or fescue species, useful for controlling plant life cycles and/or growth

Ong EK,

Emmerling

<u>;;</u>

Claim 4; Fig 49; 290pp; English

CC (I) from a regerates (Lolium Sp.) or fescue (Festuca Sp.) species, such as CC MADS-box (MADS) and MADS-like proteins, CENYRORADIALIS (CEN) and CEN-like proteins, A PETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) CC and HB-like proteins, or their functionally active fragments or variants. CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a construct (III) comprising construct (III) comprising and plant. The construction of construction of construction of construction and growth or alter flower corporation of construction and growth or alter flower corporation of construction and growth or alter flower ing. CC change, flowering time and the number of leaves made before flowering. CC change, flowering time and the number of leaves made before flowering. CC change, flowering time and flowering architecture. Manipulation of construction of construction of construction construction of construction construction. This seed production, changing flower construction construction involved in flowering time allowing early and construction involved in flowering and reducting construction involved in flower construction. invention describes a substantially purified or isolated polypeptide cycles

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                                                                                                                                                         Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN, CEN-like protein; APETALA2; AP2, AP2-like protein; HB; HDmeo-box protein; HB-like protein; plant growth; plant architecture; inflorescence development; flower development; embryo development; seed development; flower organ identity; phase change; male sterility; hybrid seed production; herbage quality; early maturing crop; blommass increase; branching increase; blocking flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
           19-OCT-2000; 2000AU-0000873
                                    17-OCT-2001; 2001WO-AU01311
                                                               25-APR-2002
                                                                                        WO200233091-A1
                                                                                                                   Lolium perenne
                                                                                                                                               allergenic
                                                                                                                                                                                                                                                                   Novel floral meristem identity gene LpCENa contig #3
                                                                                                                                                                                                                                                                                                 27-AUG-2002
                                                                                                                                                                                                                                                                                                                             ABK82094;
                                                                                                                                                                                                                                                                                                                                                   ABK82094 standard; cDNA;
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                                                                                                                                               floral meristem
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                                                                                                                                            identity protein;
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(AGRI-) AGRIC VICTORIA SERVICES PTY (AGRE-) AGRESEARCH LTD.
                                                                           Sawbridge
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                                                                           Ong EK,
                                                                                GLT
                                                                           Emmerling
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New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass fescue species, useful for controlling plant life cycles and/or growtphases . grass or

Claim 3; Fig 32; 290pp;

Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a C vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant CC architecture and/or flower and/or inflorescence development in a plant, CC which involves introducing (II), (III) or (IV) into the plant. The cindividual or simultaneous enhancement or downregulation of MADS-box CC gene activities may alter flower, embryo and seed development, e.g., CC enhance or inhibit embryo differentiation and growth or alter flower CC organ identity through conversion of one floral organ in another.
CC Manipulation of CEN or HB activity in plants alters the control of phase CC change, flowering time and the number of leaves made before flowering. CC Manipulation of one floral organ in another. Heads to a change in the number of floral organs and flowering architecture. Manipulation of the activity in plants alters flower organ identity through conversion of one floral organ in another. Heads to a change in the number of floral organs and flowering architecture. Manipulation of floral organs and flowering architecture manipulation of the number of floral organs and flowering architecture. flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase blomass production; increasing branching to enhanced business in fruit trees; altering plant size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This sequence represents a contiguous polynucleotide novel floral meristem identity protein involved in floral development and a potential terroit for manifulation plant. The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. development and a potential target for manipulating plant life cycles.

Sequence 787 BP; 194 A; 180 C; 179 G; 228 T; 6 other;

Query Match Best Local Matches Local Sinhes 311; Similarity Conservative 20.4%; Score 175; DB 24; Pred. No. 2.4e-31; 0; Mismatches 206; Length Indels u ! Gaps ۲:

Ş 밁 Q 320 CGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGC 625 260 AAGCCATCTAAAGTCTTCCTTCCTCCGCAGCCACTCTCCCTCTGACAATTGTAGAAAACTG 319 379

565 CAGCCACAGGGAGGCCAAGATCATTATCCACAGCAAACTGGCGGGTGTTGAAATGATCCC 506

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밁 Q 505 380 TGAAGGAAGGCACAGATACAGTCTGCCTTCGCTTNTGCTTGAAGAGCACAAAAATGAACC GCCACCCTGGTGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGACAC 439 446

δÃ 440 499

멍 ρ 밁 385 445 500 CATCTGTTGTCCCAGGTATATTACTGACAATCCAGTGAAGATGCTCCCGCAGATACGGAT TTCCAGTTGTAGCAGGGATATCAGTCACCAACCAATGGAGATATTCTCGGAGGTGAGGGT TGTGGATTCCAATGTTGGGCTTTGGGCTCTCATAGCTCATGACCTCCCCCCCAAATGAAG 559 386

Š 560 TGCTAGGACTTGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGAGGTCTT 619

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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 292; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the nucleic acid and protein sequences of a number of proteins from the strawberry which are involved in the regulation of flowering. These were identified using primers based on the homologous sequences from A. thaliana, B. napus and R. sativus. They can be used in the production of transgenic field crops whose flowering is regulated and the time of fruiting and harvesting can be manipulated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strawberry; flowering regulation; harvesting; fruit production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid involved in controlling plant flowering processes useful for generating transgenic plants, in particular strawberry plants having altered flowering behavior such as early, delayed or day-neutral flowering
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                                                                                                                                                                                                                                                                                                                                                             Sequence
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                              337 AGATTGTAGATCTCAGCAAACTCGCGAGTGTTGTAAGTTCTGGCGCGCCACCCTGGTGCATAC 396
                                                                                                               515 CGTCTTCTTGCTGCCGTTTCTCTCTGTGCATTGAAGTAAACGGCAGCAACAACACCCA 456
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CTTCCAACAGCTAGAGGTTCCGACATTCTT 6
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SUMMARIES

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206	231.6	234	423	494		Score
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ALIGNMENTS

	FEATURES source			JOURNAL		AUTHORS	REFERENCE			MSIN		S	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AV563203
/organism="Arabidopsis thaliana" /strain="Columbia"	Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers 1518	The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan	Contact: Erika Asamizu	DNA Res. 7, 175-180 (2000)	of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation	1 (bases 1 to 518)	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	thale cress.	EST.	AV563203.1 GI:8734629	AV563203	AV563203 Arabidopsis thaliana green siliques Columbia Arabidopsis	AV563203 518 bp mRNA linear EST 07-SEP-2000	

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                                   DNA Res.
20363093
                                       Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries DNA Res. 7, 175-180 (2000)
            Contact: Erika Asamizu
The First Laboratory f
                                                                                            1 (bases 1 to 494)
Asamizu, E., Nakamura, Y.,
                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; euroside; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone="SQ183b01F"
/clone_lib="Arabidopsis thaliana green
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_
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 Laboratory Research
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Pred. No. 1.9e-79;
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REFERENCE AUTHORS

1 (bases 1 to 423) Seki,M., Narusaka,M., Ishida,J., F Oono,Y. Sakurai,T., Carninci,P., Arakawa,T., Shibata,K., Shinagawa,

Ishida, J., Kamiya, A., Carninci, P., Kawai, J., C., Shinagawa, A., Murama

Muramatsu,

Hayashizaki, Y

Nakajima, M.,

Itoh, M., Satou, M., Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

SOURCE ORGANISM

Arabidopsis thaliana thale cress

KEYWORDS VERSION ACCESSION

AV788551.1 EST.

GI:19807341

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AV788551 RAFL6
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Email: asamizu@kazusa.or.jp,
Location/Qualifiers
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xhoI"
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ169b07F"
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/tissue_type="green siliques"
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Pred. No. 1.4e-75;
D; Mismatches 0;
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     BE590867 551 bp WHE0855_C01_E012S Wheat 20-45 DA aestivum cDNA clone WHE0855_C01_BE590867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An Arabidopsis full-length CDNA library was constructed essentially as reported previously (Sek1 et al., 1998). This clone is in a modified pBluescript vector as a SstI/KhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-298-36-9060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mseki@rtc.riken.go.jp
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/db_xref="taxon:3702"
/clone="RAFL06-80-B19"
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614 GGTCTTCTCCACCAATCTCAACTCTTGGCTTGTTTTGAACCTGAGAAGGCCTTAGATCCA
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                                                                                                                                                                                                                                                                                                                                                       314 AAACTGCGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGT 373
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                                                                                      GAGGGTTGCTAGGACCTTGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGA
                                                                                                                         AGGATGCACCAGTTGTACCGGGGATATCTGTCACAAGCCAGTGGAGATACTCCCTAAGGT
                                                                                                                                                                                            CGAAGCGATGGATCCCCATGGTCGGACGAGGGCTCTCGTAGCACATCACCTCCTGCCCGA
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1 (bases 1 to 551)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., He,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: oandersn@pw.usda.gov
Sequence have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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5105595818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone="WHE0855_COL_EO1"
/Clone="WHE0855_COL_EO1"
/Clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared, a
cDNA library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
(Choi, Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="Chinese Spring"
/db_xref="taxon:4565"
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Location/Qualifiers
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 CCTGCAGTGGGACTTGGATTTTCGTAACACACAATCTCATTGCCAAAGGTTGTTCCAGTT
                                                                                                        GGAAGGCCGAGATTGTAGATCTCAGCAAACTCCGCGAGTGTTGAAGTTCTGGCGCCCACCCT 387
                              GGTGCATACACTGTCTGCCTACCCAGTTGGCGAAACAATACAAAAACAAAGCGATGAATC
                                               GGTGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGACACGATGAATT
                                                                                         GGCAAACCAAGATTATAAAGCTCAGCAAAGTCCCTAGTGTTGAAATTTTGGCGCCACCCT 389
                                                                                                                                                  TATGATCTTCGACCACCCGAGCCGCCCTCCCTTTGGCAGTTAAAATAAACAGCAGCAACA 329
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                                                                                                                                                                                                                291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unite de Recherche des Produits de la Vigne Institut National de la Recherche Agronomique 2, place Viala, 34 060 Montpellier Cedex 01, 1 Tel: 00-33-(0)4-99-61-28-62 Fax: 00-33-(0)4-99-61-28-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimple Hamdl, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ797327 659 bp EST 6265 Ripening Grape berries I vinifera cDNA clone RT071D11 3', BQ797327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: romieu@ensam.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Romieu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
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                                                                                                                                                                                                                                                                                                              /clone_lib="Ripening Grape berries Lambda Zap II Library" /dev_stage="ripening stage"
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco Ri; Site_2: XhOI; Oriented library, construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier, N., Ageorges, A., Abbal, P., Romieu, C. in J. plant physiol. 158
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:29760"
/clone="RT071D11"
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Lambda Zap II Library Vitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 206)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                             Similarity 100.
06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332-3, Kisarazu, Chiba 292-0812, Japan
asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 bp mRNA linear EST 07-SEP-20 Arabidopsis thaliana green siliques Columbia Arabidopsis CDNA clone SQ134d05F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Arabidopsis thaliana green siliques
/tissue_type="green siliques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/clone="SQ134d05F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescriptII SK-;
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1 (bases 1 to 1168)
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Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Mapping Project 159 t 336 others
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Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
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Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fe, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Seaton, C.L. and Tong, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE498304 505 bp mRNA linear EST 04-AUG-2000 WHE0963_B10_C19ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0963_B10_C19, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: Stratagene SK primer.
Location/Qualifiers
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                                                                            greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside, Plasmid DNA
                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR, excised phage
Site_1: EcoRI; Site_2: XhoI; Plants were grown
                                    Anderson lab
                                                        preparations
                                                                                                                                                                                                                                                                                                                                                           /cultivar="Chinese Spring'/db_xref="taxon:4565"
                                                                                                                                                                                                                                                   /dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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Query Match Best Local Similarity

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Score 198.4; DB 10; Pred. No. 8.4e-25;

Length 505

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                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
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                                                                                                                                                                                                                                                        Email: oandersn@pw.usda.gov
Sequence have been trlmmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 491)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fe,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
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/db_xref="taxon:4565"
/clone="WHE2314_C03_E06"
         /note="Vector:
Site_1: EcoRI;
                                                 /clone_lib="Wheat pre-anthesis spike
/tlssue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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Barley EST sequencing project in Unpublished (2002) AV937451 K. Sato unpublished cDNA library, heading stage top three leaves Hordeum vulg cDNA clone bahlln08 5', mRNA sequence AV937451 National Institute of Genetics 1111 Yata, Mishima, Shizuoka 4 Tel: 81-559-81-6856 Fax: 81-559-81-6855 Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Center For Genetic Resource Information Contact: Tadasu Shin-i Spermatophyta; Magnoliophyta; AV937451.1 GI:18233248 Triticeae; Hordeum. (bases 1 to 542) Location/Qualifiers /organism="Hordeum vulgare /strain="H602" Liliopsida; NIG subsp. and vulgare subsp. spontaneum Embryophyta; Tracheophyta; a; Poales; Poaceae; Pooldea Okayama spontaneum" linear EST 18-JAN-2002 strain H602 adult, Univ Pooldeae

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                                                                                                                                                                                                                             mRNA sequence.
BG647258
BG647258.1 GI:
                                                 Hahn,M.G., Ojanen-Reuhs,T., Samac,D., 1
Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula
oligogalacturonides of DP 6-20
                         Unpublished (2001)
Contact: Michael G. Hahn
                                                                                                                                      Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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EST508867 HOGA Medicago
University of Georgia
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/clone="bahlin08"
/clone="bahlin08"
/clone="bahlin08"
/clone="says to unpublished cDNA library, adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult; heading stage"
150 c 146 g 124 t 2 others
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                                                                  TAAAGGAATCAAGAACTTCTCCTATCACTCTTCCAACAATGAGTGGTTCTTGAGACATTC
                                                                                                    TAAACGGATCAAGAACGTCTCCAACAACTCTGCTTACTATAAGAGGGTCTCTTATATTTA
                                                                                                                                                      TCCTGAGGTCTTCTCCACCCAATCTCAACTCTTGGCTTGTTTTTGAACCTGAGAAGGCCTTA
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Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
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Tel: 706-542-4457
Fax: 706-542-4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hahn@ccrc.uga.edu
G390854e TIGR sequence name:
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/note-"Nector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

a 147 c 150 g 241 t
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/dev_stage="24 hours after treatment in the with 0.5 mg/ml oligogalacturonides (DP 6-20)
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
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/clone="pHOGA-1619"
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                                                                                                                                                                                                                                                                                                                                                                                              273 TCTTCTTCCTCCGCAGCCACTCTCCCTCTGACAATTGTAGAAAACTGCGGCCACGGGAAG 332
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                               TGGAACATCTGGATCCACCATAACCAAAGTATAGAAGTTCCTGAGGTCTTCTCCACCAAT
                                                                                         AGCAGGGATATCAGTCACCAACCAATGGAGATATTCTCGGAGGTGAGGGTTGCTAGGACT
                                                                                                                                        GATCACTGGTTTTGGACTATCGTAGCTCACTATCTCTTTTCCAAAAGAAGCATCAGTTGA
                                                                   TGGAACATCTGGATCAGTGATGAGTGTATAAGCAGATCTCATGTCTTCACCACCAAT
                                                                                                                                                            TGCAGTGGGACTTGGATTTTCGTAACACACAATCTCATTGCCAAAGGTTGTTCCAGTTGT
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Generation of ESTs from potato roots
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1 (bases 1 to 718)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone info: please contact Research Genetics, Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Utterback, T., Chiemingo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van der Hoeven, R.,
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Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(-); Site_1: EcoRI;
XhoI; supplier: Cornell University, Tanksley lab
sequencing; The Institute for Genomic Research. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="potato roots"
/tlssue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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Pred. No. 1.5e-20;
0; Mismatches 208;
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, Bougri,O., Buell,C.R., Ro;
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                                                                      GTGGGACTTGGATTTTCGTAACACACACAATCTCATTGCCAAAGGTTGTTCCAGTTGTAGCA
                GGGATATCAGTCACCCAACGAGGAGATATTCTCGGAGGTGAGGGTTGCTAGGACTTGGA
                                                                                                                     AAAACTGTACCCCTGCCTAGTTGCTGGAACAGCACAAATACCATCCGGTGGATACCAGAT
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BJ453783 K. Sato unpublished cDNA librar
vegetative stage leaves Hordeum vulgare
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center For Genetic Resource Information National Institute of Genetics
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato, K.,
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81-559-81-6855
                                                                                                                                                                                                                                                                                                                                   Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saisho, D. and Takeda, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="K. Sato unpublished cDNA
Akashinriki vegetative stage leaves"
/tissue_type="leaves"
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114 c 129 g 123 t
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/cultivar="Akashinriki"
/db_xref="taxon:112509"
/clone="baak44h08"
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                   TGCATACACTGTTTGCCTGCCAAGCTGTCGAAACAATATAAACACGGCACGATGAATTCC 449
                                                                                   AAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTGTTGAAGTTCTGGCGCCACCCTGG 389
                                                                                                                                 AAACCTTCTTCCGCCTGATCCACCTTCCCTTTGACA---GTTGAAATATGAGGCAGCCAC 445
                                                                                                                                                                  AAGTCTTCTTCCTCCGCAGCCACTCTCCCTCTGACAATTGTAGAAAACTGCGGCCACGGG 329
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TGCAAAAACTGTACCCCTGCCTAGTTGCTGGAACAGCACAAATACCATCCGGTGGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BJ448552 K. Sato unpublished cDNA library, cv. vegetative stage leaves Hordeum vulgare subsp. baak20f16 5', mRNA sequence.
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Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
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                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /clone_lib="K. Sato unpublished cDNA Akashinriki vegetative stage leaves" /tissue_type="leaves"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                   /dev_stage="vegetative stage"
142 c 166 g 173 t
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Pred. No. 6e-19;
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JOURNAL
Query Match
Best Local Similarity 59.0
Matches 289; Conservative
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BJ315664 Y. Ogihara unpublished
aestivum cDNA clone whyf19i17 5'
BJ315664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center For Genetic Resource Information National Institute of Genetics Ill1 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in Triticum Unpublished (2002)
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Ogihara, Y. and Murai, K.
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; Triticeae; Triticum.
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                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                             hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dovark Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo
                                                                                                      Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).

Plasmid DNA preparations and DNA sequencing were performed in the OD Andersson lab (all other authors)."

151 c 143 g 147 t 3 others
                                                                                                                                                                                     excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chi
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Y. Ogihara unpublished cDNA library, Wh_1/tissue_type="spikelet at early flowering"
/dev_stage="Feekes' scale 6"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="whyf19i17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Triticum aestivum'
                       18.4%;
    0;
    Score 157.2; DB 1
Pred. No. 9.4e-18;
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cDNA library, Wh_yf Triticum
                                            DB 13;
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                                                                                   590 TAACCAAAGTATAGAAGTTCCTGAGGTCTTCTCCCACCAATCTCAACTCTTGGCTTTTT 649
                                                                                                     767 TAAGAGGGTC 776
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92 TAAGAGGTTC 83
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Search completed: May 2, 2003, 11:50:32 Job time: 1785.5 secs

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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Backfiles1.seq:*
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US-08-467-9478-3
US-08-468-4510-60
US-08-488-2110-60
US-08-906-616-60
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ALIGNMENTS

AND GENETICALLY
MODULATED FLOWER DEVELOPMENT

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APPLICANT: Weigel, Detlef
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT) ANT
TITLE OF INVENTION: MODIFIED PLANTS HAVING MOI
FILE REFERENCE: SALKINS.026A
CURRENT APPLICATION NUMBER: US/09/060,726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOTS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 856
TYPE: DNA
ORGANISM. Arabidopsis thaliana
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Matches 856;
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CGAGTGTTGAAGTTCTGGCGCCCACCCTGGTGCATACACTGTTTGCCCTGCCAAGCTGTCGA
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                                                  TGACAATTGTAGAAAACTGCGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCG
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Pred. No. 3e-217;
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TITLE OF INVENTION: FLOWERING LOCUS T (FT) A
TITLE OF INVENTION: FLOWERING LOCUS T (FT) A
FILE REFERENCE: SALKINS.026A
CURRENT APPLICATION NUMBER: US/09/060,726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 855
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Patent No. 6225530
GENERAL INFORMATION:
APPLICANT: Weigel, Detlef
APPLICANT: Salk Institute
                                                                                             Matches
                                                                                                   Query Match
Best Local Similarity
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                                                                                                                          NAME/KEY: CDS
LOCATION: (63)...(590)
-09-060-726A-1
                                                                                                                                                LENGTH: 855
TYPE: DNA
ORGANISM: Arabidopsis
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

Version

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25

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: CUSHMAN, DARBY &
ADDRESSES: CUSHMAN, DARBY &
ADDRESSES: CUSHMAN, DARBY &

STREET: 1615 L. CITY: Washington STATE: D.C.

COUNTRY: USA ZIP: 20036

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RESULT 3
US-07-644-372-1/c
                                                    Sequence 1, Application US/07644372 Patent No. 5416009
                                            Patent No. 5416009
GENERAL INFORMATION:
APPLICANT: Lazzeri, Mario E.
APPLICANT: Nutman, Thomas B.
APPLICANT: Weiss, Niklaus
TITLE OF INVENTION: A DNA SEGMENT ENCODING A
TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
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CURRENT APPLICATION DATA:

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; LOCATION:
US-07-644-372-1
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Best Local Similarity
                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                         Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS LENGTH: 822 base pairs
                                                            TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
                               CORRESPONDENCE ADDRESS:
                                                                                                APPLICANT:
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19910:
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                                                                                                                                                                                                                             , Application US/08467948A
5998164
                                                                                                                                                            CAO, LIAN
: STERNE, KESSLER,
1100 NEW YORK AVE.,
                                                                                           GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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52..507
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51.3%;
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Pred. No. 5.8e-10;
GOLDSTEIN & FOX P.L.L.C NW, SUITE 600
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; LOCATION:
US-08-467-948A-3
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2018
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                                                                                   COMPUTER READABLE FORM:
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            SOFTWARE: PATENTIN REI
CURRENT APPLICATION DATA:
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      IIILE OF INVENTION: Polynucleotides Encoding Human G-Protein
IIILE OF INVENTION: Coupled Receptor GPR1
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              802 CTTGAACAAACCTCGTGCTGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGA 856
                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
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                                                                                                                                          ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE., CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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REFERENCE/DOCKET NUMBER:
                                                                       MEDIUM TYPE:
                                                                                                      COUNTRY: UZIP: 20005
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50; Conserv
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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                                                                         FLOPPY DISK
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90.9%;
US/08/467,947A
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US-08-467-947A-3
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Best Local Similarity 90.9%;
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                                                                  APPLICATION NUMBER: US/08/485,455D FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J. REGISTRATION NUMBER: 32,020 REFERENCE/DOCKET NUMBER: 2618-25-C1-3 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                 TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
NAME: STEFFE, 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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LENGTH:
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o. 5712143
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Rushlow, Keith E.
Wu Hunter, Shirley
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884..2062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Gary L.
FLEA PROTEASE PROTEINS, NUCLEIC ACID
MOLECULES, AND USES THEREOF
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                                                                                                            2618-25-C1-3
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US-08-485-455D-60
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Best Local Similarity 73.2%;
Matches 60; Conservative
             Query Match
Best Local Similarity
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   Matches '60;
                                                                                                                                                                                             TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                        TELEPHONE: (303) 863-9700
                                                                                                        FEATURE:
                                                                                                                        MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
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FEATURE:
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CITY: Denver
STATE: Colora
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                                                                         NAME/KEY: CDS
LOCATION: 1..
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/482,130C FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 80203
                                                                                                                                      TOPOLOGY:
                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                               LENGTH:
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5962257
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                                                                                                                                                                 nucleic acid
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                                                                                                                                                                              234 base pairs
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   Conservative
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                                                                                                                                      linear
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                5.5%;
73.2%;
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Score 46.8; DB 2;
Pred. No. 0.0015;
0; Mismatches 22;
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Pred. No. 0.0015;
0; Mismatches 22;
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                           Length 234;
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RESULT 9
US-08-906-769-60/c
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,211C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION UNMBER: 32,020
REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID TITLE OF INVENTION: MOLECULES, AND USES THEREOF NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
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                                                                                                              835 CGGGGGATCCACTAGTTCTAGA 856
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                                                                                                                                              129 TATCTTGTAAGATGAGACGCGCTCAATCCAACCAAACGCTCGTGCCGAATTCCTGCAGCC 70
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LOCATION: 1..
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CITY: Denver
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                                                                                CGGGGGATCCACTAGTTCTAGA 48
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Pred. No. 0.0015;
0; Mismatches 22;
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Patent No. GENERAL II

INFORMATION:

APPLICANT:
APPLICANT:

Grieve, Robert B. Rushlow, Keith E.

Wu Hunter, Shirley Frank, Glenn R.

APPLICANT:

APPLICANT:

Sequence 60, Application US/08906616 Patent No. 6121035

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RESULT 10
US-08-906-616-60/c
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Matches
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
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                                                       775 TCTCTTATTATTATAGACATCTTTGATCTTGAACCAAACCTCGTGCTGAATTTCCTGCAGCC 834
                                                                                                                                                                        Local Similarity 73.2
les 60; Conservative
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TOPOLOGY: lin
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                 TATCTTGTAAGATGAGACGCGCTCAATCCAACCAAACGCTCGTGCCGAATTCCTGCAGCC 70
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                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                               1..234
                                                                                                                                                                                                                                                                                                     linear
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.0015;
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Best Local Similarity
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                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
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APPLICANT:
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LENGTH: 234 base pairs
TYPE: nucleic acid
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                                                TITLE OF INVENTION:
                                                                             TITLE OF INVENTION:
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                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 TCTCTTATATTTATAGACATCTTTGATCTTGAACAAACCTCGTGCTGAATTCCTGCAGCC 834
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LICANT: Silver, Gary
LE OF INVENTION: FLE
                                                                                                                                                                                                                                                                                                                                                                       CGGGGGATCCACTAGTTCTAGA 48
                                                                                                                                                                                                                                                          INFORMATION:
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6139840
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                        Stiegler, Gary
VENTION: USE OF PROTEASE INHIBITORS AND
VENTION: PROTEASE VACCINES TO PROTECT &
VENTION: INFESTATION, AND FLEA PROTEASE
VENTION: MOLECULES, AND USES THEREOF
EQUENCES: 119
                                                                                                                                                                                                                          Grieve, Robert B. Rushlow, Keith E.
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                                                                                                                                                                             Heath, Andrew W.
                                                                                                                                                                                         Frank, Glenn R
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                                                                                                                                                           Yamaka, Miles Yamanaka
                                                                                                                                                                                                             Hunter, Shirley Wu
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SYSTEM: PC-DOS/MS-DOS
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Sheridan Ross & McIntosh
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)N: 536
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73.2%;
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                                                             FLEA PROTEASE PROTEINS, NUCLEIC ACID
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                                                                               ANIMALS FROM FLEA
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RESULT 12
US-08-485-4438-60/c
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US-08-817-795-60
COUNTRA.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
""""FTFM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                     CORRESPONDENCE ADDRESS
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APPLICATION NUMBER: PCT/US95/14442
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              835 CGGGGGATCCACTAGTTCTAGA 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   775 TCTCTTATATTTATAGACATCTTTGATCTTGAACAAACCTCGTGCTGCATTCCTGCAGCC 834.
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                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                           CITY: DENVER
                                                                                                                                          STREET:
                                                                                                                                                          ADDRESSEE: SHERIDAN ROSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/817,795
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NO. 6146870
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                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                          1700 LINCOLN ST.,
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Hunter, Shirley Wu
Frank, Glenn R.
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(303 863-0223
                                                                                                                                                                                                                                 Stiegler,
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SYSTEM: PC-DOS/MS-DOS
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73.2%;
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FLEA PROTEASE PROTEINS, NUCLEIC ACID
MOLECULES AND USES THEREOF
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                                                                                                                                            SUITE 3500
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Pred. No. 0.0015;
0; M1smatches 22;
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Best Local (
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Patent No. 6150125
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                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID TITLE OF INVENTION: MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 190
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NAME: CONDELL, GATY L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26.
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                               ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 TATCTTGTAAGATGAGACGCGCTCAATCCAACCAAACGCTCGTGCCGAATTCCTGCAGCC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 TCTCTTATATTATAGACATCTTTGATCTTGAACAAACCTCGTGCTGAATTCCTGCAGCC 834
                                                               APPLICATION NUMBER: US/08/639,075A FILING DATE: 24-APR-1996 CLASSIFICATION: 424
            NAME: Connell, Gary J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                           CITY:
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les 60; Conserv
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LOCATION: 1...
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CLASSIFICATION:
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                                                                                                                                                                                                                          ZIP: 80203
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                             Silver, Gary
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              32,020
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Pred. No. 0
2618-25-C2
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RESULT 14
US-09-012-431-60/c
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; LOCATION:
US-08-639-075A-60
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                                                       INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
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Local Similarity 73.2%;
nes 60; Conservative
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STRANDEDNESS: single
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                                                                                                                           APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COnnell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), Application US/09012431 6180383
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/012,431 FILING DATE: 23-Jan-1998
LENGTH: 234 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1700 Lincoln Street, Suite 3500
                                                                                            TELEFAX: (303) 863-0223
                                                                                                               TELEPHONE: (303)
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Silver, Gary
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863-0223
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Pred. No. 0.0015;
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US-09-012-692-60/c
                                                                                                                                                            NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 35,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.5%;
Best Local Similarity 73.2%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDING
STREET: 1/C
CITY: Denver
COlorado
TYPE: Colorado
                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: SIlver, Gary
ITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
ITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1..234
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
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                                                                                                                         234 base pairs
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Pred. No. 0.0015;
0; Mismatches 22;
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Search completed: May 1, 2003, 21:56:17 Job time : 64 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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US-09-938-842A-1501
US-09-948-842A-1380
US-10-092-164-380
US-10-074-095-248
US-10-074-095-248
US-09-764-860-248
US-09-764-868-303
US-09-764-891-404
US-09-925-297-400
US-09-925-299-270
US-09-925-299-270
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US-09-291-809C-3
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Sequence 2635, Ap
Sequence 6398, Ap
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O; Indels O; Gaps	TICALLY DEVELOPMENT	·	Sequence 3, Appli Sequence 309, App Sequence 309, App Sequence 352, App Sequence 352, App Sequence 352, App Sequence 78, Appli Sequence 78, Appl Sequence 29, Appl Sequence 103, App Sequence 11, App Sequence 417, App Sequence 418, Appl Sequence 184, Appl Sequence 36, Appl Sequence 374, App Sequence 374, App Sequence 3774, App Sequence 3774, App Sequence 3774, App Sequence 376, Appl Sequence 3774, App Sequence 3774, App
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                                                    PRIOR APPLICATION NUMBER: PCT/U
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 09/06
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows V
                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                               Sequence 3, Application US/09291809C Patent No. US20010049831A1
                                            SEQ ID NO 3
TYPE: DNA
ORGANISM: Arabidopsis
-09-291-809C-3
                                                                                                                     FILE REFERENCE: SALKINS.026CP1
CURRENT APPLICATION NUMBER: US/09/291,809C
CURRENT FILING DATE: 1999-04-14
                                                                                                                                                       APPLICANT: Detlef Weigel
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT)
TITLE OF INVENTION: MODIFIED PLANTS HAVING
                                LENGTH:
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RESULT 3 US-09-845-849-1/c

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GENERAL INFORMATION:

APPLICANT: THE SALK INSTITUTE APPLICANT: WEIGEL, Detlef

FOR

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Sequence 1, Application US/09845849 Patent No. US20020029395A1

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Pred. No. 9e-206;
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Best Local Similarity
Matches 856; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWI
FILE REFERENCE: SALKINS. 0260V1
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR APPLICATION NUMBER: 09/060,726
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TYPE: DNA
ORGANISM: Arabidopsis
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                                    GATCTATTAAACGGATCAAGAACGTCTCCCAACAACTCTGCTTACTATAAGAGGGGTCTCTT
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Pred. No. 9e-206;
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LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWF
FILE REFERENCE: SALKINS.026DV1
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
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TATTCTCGGAGGTGAGGGTTGCTAGGACTTGGAACATCTGGATCCACCATAACCAAAGTA
                             TGACAATTGTAGAAAACTGCGGCCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTCG
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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR REPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR REPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2635
LENGTH: 528
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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APPLICANT: Kreps, Joel
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GGTGGCAGGTATATCAGTCACCAACCAGTGGAGATATTCTCGTTGAGGGTTGCTTGG
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Pred. No. 2.1e-85;
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APPLICANT: HATPER, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Day, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1501
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US-09-938-842A-1501/c
Sequence 1501, Application
Patent No. US20020160378A1
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LENGTH: 534
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                                                                                                                                                                                                     GCTTCTGCCTGAACAGAACAAACACAAACCTATGTATCCCTATGCTTGGCCTTGGCAATT
TCACCAAAGTGAAGAAGGATCTGAGATCACCACGATGGATCTCAACCCTAGGCTTGGAGG
                            TAACCAAAGTATAGAAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTTGGCTTGTTTT 649
                                                               TCCAGTGCAGGTGTTCTTTAGAAAGGGGTCACTAGGACCTGGAACATCTGGGTCTATCA
                                                                                  ACCAATGGAGATATTCTCGGAGGTGAGGGTTGCTAGGACCTTGGAACATCTGGATCCACCA 589
                                                                                                                                CATAGCTCACCACCTCTTTGCCAAACGTAGCATCTGTTGTGCCGGGAATGTTTGTAACGA
                                                                                                                                                     CGTAACACACAATCTCATTGCCAAAGGTTGTTCCAGTTGTAGCAGGGATATCAGTCACCA 529
                                                                                                                                                                                                                        CAAGCTGTCGAAACAATATAAACACGACACGATGAATTCCTGCAGTGGGACTTGGATTTT
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Pred. No. 7.8
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RESULT 8
US-10-092-154-380/c
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098321H1
US-09-878-574-6398
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TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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                                                                                                                              Sequence 380, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
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LENGTH: 251
Prior Application removed -
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 380
LENGTH: 503
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Best Local :
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                                                                                             CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
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APPLICANT:
                                                                           NUMBER OF SEQ ID NOS: 2003
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                                                     See File Wrapper or Palm
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Pred. No. 3.7e-09
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                                                  US-09-764-847-380
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 380, Application US/09764847 Patent No. US20020132767A1 GENERAL INFORMATION:
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   Matches
                           Query Match
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                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                           Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 2003
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
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                                                                                                                                                                                                              LOCATION: (20)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                           TYPE: DNA
                                                               OTHER INFORMATION: n
                                                                                     NAME/KEY: SITE
                                                                                                    OTHER INFORMATION: n
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                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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OTHER INFORMATION: n equals
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                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (29)
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               Local
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  1 Similarity
57; Conserv
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              Score 49.2;
Pred. No. 0.
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Mismatches
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              0.01;
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US-10-074-095-248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/074,095 CURRENT FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR APPLICATION NUMBER: 60/217,496
OR FILING DATE: 2000-07-11
OR APPLICATION NUMBER: 60/225,447
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/218,290
OR FILING DATE: 2000-07-14
OR APPLICATION NUMBER: 60/225,757
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/226,868
OR FILING DATE: 2000-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: 60/216,880
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/225,270
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/251,869
OR APPLICATION NUMBER: 60/235,834
OR APPLICATION NUMBER: 60/235,834
OR APPLICATION NUMBER: 60/235,834
OR APPLICATION DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                PR APPLICATION NUMBER: 60/234,274
R FILING DATE: 2000-09-21
PR APPLICATION NUMBER: 60/234,223
R FILING DATE: 2000-09-21
PR APPLICATION NUMBER: 60/228,924
R FILING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
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                                                                      APPLICATION NUMBER: 60/241,809 FILING DATE: 2000-10-20
                                                                                                                  APPLICATION NUMBER: 60/220,964 FILING DATE: 2000-07-26
                                                                                                                                                               APPLICATION NUMBER: 60/224,519 FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225,267 FILING DATE: 2000-08-14
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APPLICATION NUMBER:
FILING DATE: 2000-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/764,860 FILING DATE: 2001-01-17 APPLICATION NUMBER: 60/179,065 FILING DATE: 2000-01-31
    FILING DATE: APPLICATION |
                                                                                                                                                                                                           APPLICATION NUMBER: 60/236,369 FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/
FILING DATE: 2000-08-14
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                                                 APPLICATION NUMBER: 60/249, 299
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b. US20030077704A1
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OR APPLICATION NUMBER: 60/229,287
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,513
FOR APPLICATION NUMBER: 60/231,413
FOR FILING DATE: 2000-09-08
FILING DATE: 2000-09-08
                                                                                                                                                     OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,210
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/226,681
OR FILING DATE: 2000-08-22
OR APPLICATION NUMBER: 60/225,759
OR FILING DATE: 2000-08-14
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/227,113
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/227,182
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OR APPLICATION NUMBER: 60/236,802
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,037
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,040
OR FILING DATE: 2000-10-02
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/240,960
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-10-20
R APPLICATION NURSE FILING DATE: 2
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APPLICATION NUMBER: 60/241,787
APPLICATION 1000-10-20
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APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
FILING DATE: 2000-09-29
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FILING DATE: 2000-08-14
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FILING DATE: 2000-08-22
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APPLICATION NUMBER: 60/246,532
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FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,038
FILING DATE: 2000-10-02
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FILING DATE: 2000-09-01
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                                       NUMBER: 60/
: 2000-09-27
NUMBER: 60/230,438: 2000-09-06
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FILING DATE:

APPLICATION NUMBER: 60/249,208

2000-11-

60/249,218

APPLICATION NUMBER:

2000-08-14 2000-06-30

60/225,266

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER: 60/249,213

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60/249,207

APPLICATION NUMBER: 60/249,212

APPLICATION NUMBER: 60/249,245

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Best Local
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840 GATCCACTAGTTCTAGA 856
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les 59; Conserv
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FILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/231,243
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                                                                                           Conservative
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76.6%;
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                                                                                                        Score 48.2; DB Pred. No. 0.016;
                                                                                           Mismatches
                                                                                                                         9;
                                                                                           18;
                                                                                                                         Length 367;
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Conservative

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Gaps

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RESULT 12
US-09-925-300-816/c
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, NAME/KEY: SITE
; LOCATION: (345)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : SOFTWARE: Patentin Ver. 2
; SEQ ID NO 248
: LENGTH: 367
: TYPE: DNA
: ORGANISM: Homo sapiens
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US-09-764-860-248
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                                                                      ; OTHER INFORMATION: n equals US-09-925-300-816
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 816, Application US/09925300 Patent No. US20020151681A1
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Best Local (
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                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Steve Ruben TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PA101
                                                                                                                                      NAME/KEY: misc feature
LOCATION: (2)
OTHER INFORMATION: n equals
                                                                                                       NAME/KEY: misc feature LOCATION: (15)
                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                   LENGTH: 551
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75.0%;
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Score 48; DB 10; I Pred. No. 0.022; 0; Mismatches 20;
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Pred. No. 0.016;
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                                 Length 551;
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; ORGANISM: Homo sapiens
US-09-764-868-303
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SEQ ID NO 303
LENGTH: 2585
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SEQ ID NO 400
LENGTH: 560
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     Matches
                   Query Match
Best Local S
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Matches 4
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Best Local
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
                                                                                                                                           LOCATION: (7)

OTHER INFORMATION: n equals

NAME/KEY: misc feature

TOTATION: (10)

TOTATION: (10)

TOTATION: (10)

TOTATION: (10)
                                                                                                       NAME/KEY: misc feature LOCATION: (14)
                                                                                                                                     LOCATION: (10)
OTHER INFORMATION: n equals a,t,g,
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                                                                                     OTHER INFORMATION: n equals a,t,g, or
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49; Conser
                   Similarity
     Conservative
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75.6%;
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96.1%;
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Score 47.6; DB 10;
Pred. No. 0.028;
0; Mismatches 19;
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Pred. No. 0.
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LENGTH: 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC006 CURRENT APPLICATION NUMBER: US/09/764,891 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (28)
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OTHER INFORMATION: n
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NAME/KEY: SITE
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ORGANISM: Homo sapiens
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